

GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n-model

Run on: March 14, 2006, 07:44:42 ; Search time 15376 Seconds  
(without alignments)  
4898.385 Million cell updates/sec

Title: US-09-976-858-42

Perfect score: 6787

Sequence: 1 MLPVQEYKPNLQDANLCS.....MTVNTNSQNPSTLTFETAL 1325

Scoring table:

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Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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15: gb\_pl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	6787	100.0	4004	8	AY207008 Homo sapi
2	6779	99.9	4231	6	AR589389 Sequence
3	6779	99.9	4231	6	AX210645 Sequence

4	6779	99.9	4231	6	AX686744	AX686744 Sequence
5	6779	99.9	4231	8	AF071202	Homo sapi
6	6779	99.9	5832	6	CO896291	Sequence
7	6779	99.9	5871	6	CS038316	Sequence
8	6770	99.7	4515	6	CQ488793	Sequence
9	6770	99.7	4515	6	CQ490536	Sequence
10	6770	99.7	4515	6	CQ492310	Sequence
11	6770	99.7	4515	6	CQ492702	Sequence
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45	4232	62.4	4299	8	HSMB07262	Homo sapi

#### ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES
AY207008	4004 bp	Homo sapiens ATP-binding cassette transporter C4 (ABCC4) mRNA, complete cds.	AY207008	GI:31322320		Homo sapiens (human)		Submitted (24-DEC-2002)	Kato, R. and Ishikawa, T.	Department of Biomolecular Engineering, Graduate School of Bioscience and Biotechnology, Tokyo Institute of Technology, 4259 Nagatsuta-cho, Midori-ku, Yokohama-shi, Kanagawa 226-8501, Japan		1..4004 Location/Qualifiers /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /cfeature_type="kidney" 1..4004

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## ORIGIN

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US-09-976-858-42 (1-1325) x AY207008 (1-4004)

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QY 81 ThrArgAlaIleIleIysCySerTyrTrpIysSerTyrLeuValIleuGlyIlePheThrLeu 100
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QY 121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaThrVal 140
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QY 181 LeuSerAsnMetAlaMetGlyIlySerThrThrGlyGlnIleValAsnLeuLeuSerAsn 200
DB 546 CTTACTTAACATGCGCCATGCGGAGAGCAACACAGCCCGAATGATCAATCTGCTGCATAT 605
QY 201 AspValaLeuIysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
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QY 221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGlnIleGlyIleSerCysLeuAlaGly 240
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RESULT 2  
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LOCUS Sequence 1 from patent US 6803184.  
DEFINITION AR589389  
ACCESSION AR589389  
VERSION AR589389.1 GI:56636669  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 4231)  
AUTHORS Krush, G. and Lee, K.  
TITLE MPR-related ABC transporter encoding nucleic acids and methods of use thereof  
JOURNAL Patent: US 6803184-A 1 12-OCT-2004;  
Fox Chase Cancer Center: Philadelphia, PA  
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US-09-976-858-42 (1-1325) x AR589389 (1-4231)

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Qy 21 ArgValPhePheTyrTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGln 40  
Db 176 CCGCGTCTCTTCTGGGTGCTCAATCCCTGTTTAAATTGGCCATTAACGAGATTAGAG 235  
Qy 41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60  
Db 236 GAGAGATGATATGATTTCACTGTGCTGCAGAGAACCCGCTCAAGACCTTGGAGAGGAGTGG 295  
Qy 61 GlnGlyPheTyrAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80  
Db 296 CAGGGCTTTCGGATTAAGAGATTTTAAGCTGAGATGACGACAGAGGCCCTTCTTA 355  
Qy 81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyLysPheThrLeu 100  
Db 356 ACAAGAGCAATCATTAAGTTACTGGAATCTTAATTAGTTTGGGAATTTTACGTTA 415  
Qy 101 IleGluGluSerAlaLysValIleGlnProLysPheLeuGlyLysIleIleAsnTyrPhe 120

Db 416 ATTGAGAAAGTCCAAAGTAATCCAGCCCATATTTTGGGAAAAATTATTAATTTT 475  
Qy 121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140  
Db 476 GAAATTTATGATCCATGGAATCTGTGGCTTTGAACACAGGCTACGCCATATCCACGGGTG 535  
Qy 141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisIleLeuTyrPheTyrHisValGln 160  
Db 536 CTGACTTTTGGACCCCTCAATTTGGCTATACGTACCTTAATATTTTATCACTTCAG 595  
Qy 161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180  
Db 596 TGTGCTGGATGAGGTTTACAGTACCCATGTGCCATATGATTTATTCGAGGACATTCGT 655  
Qy 181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuSerAsn 200  
Db 656 CTTATTAACATGCGCATGGGAGAACCAACAGCCAGATGTCATCTGCTGCCAT 715  
Qy 201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220  
Db 716 GATGTGAACAAGTTTGATCAGGTGACAGTGTCTTACACTTCTGTGGGACAGCACCTG 775  
Qy 221 GlnAlaIleAlaValThrAlaLeuLeuThrPheGluIleGlyLysSerCysLeuAlaGly 240  
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QY 461 GlnProTPrValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysIleTyrGlu 500  
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QY 521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540  
Db 1676 GAGGATGGGATCTGACTGTGTAGAGATCGGGAAACCACTGATGAGGGGAGAA 1735  
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DEFINITION Sequence 287 from Patent WO0157058.
ACCESSION  AX210645
VERSION     AX210645.1 GI:15424905
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE   1
AUTHORS     Rosenthal, A., Hinzmann, B., Schaefer, R., Zuber, J., Tcherntseva, O.,
            Gribs, M., Hellriegel, M., Schmitz, A.C. and Sers, C.
TITLE       Detection of differential gene expression
JOURNAL     Patent: WO 0157058-A 287 09-AUG-2001;
            Metagen Gesellschaft fuer Genomforschung mbH (DE)
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                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"
ORIGIN
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Pred. No.: 0 Length: 4231
Score: 6779.00 Matches: 1323
Percent Similarity: 99.9% Conservative: 1
Best Local Similarity: 99.8% Mismatches: 1
Query Match: 99.9% Indels: 0
DB: 6 Gaps: 0

US-09-976-858-42 (1-1325) x AX210645 (1-4231)
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Db      116 ATGCTCCCGCTGACCAAGAGGTGAAGCCCAACCCGCTGACGAGCCGGAACATCTCTCA 175
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Qy      21 ArgValPhePheTrpTrpLeuAnProLeuPheLyileGIyHiscLyArgArgLeuGlu 40
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1 (bases 1 to 4231)  
Lee,K., Belinsky,M.G., Bell,D.W., Teesta,J.R. and Krub,G.D.:  
Isolation of MOAT-B, a widely expressed multidrug  
resistance-associated protein/canicular multispecific organic  
anion transporter-related transporter  
Cancer Res. 58 (13), 2741-2747 (1998)  
JOURNAL  
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Submitted (09-JUN-1998) Medical Oncology, Fox Chase Cancer Center,  
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ORIGIN



## Alignment Scores:

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US-09-976-858-42 (1-1325) x AF071202 (1-4231)

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 Homnidae; Homo.  
 REFERENCE 1

AUTHORS Hinzmann, B., Dahl, E., Rosenthal, A., Specht, T., Schmitt, A., Beckmann, G., Brummetendorf, T., Kimmennann, H., Roepcke, S., Hermann, K., Kitzhong, L., Pflaerke, C. and Staub, E.  
 TITLE Human nucleic acid sequences obtained from prostatic carcinomas  
 JOURNAL Patent: WO 2004/076614-A 115 10-SEP-2004;  
 Hinzmann, Bernd (DB); Dahl, Edgar (DB); Rosenthal, Andre (DB); Specht, Thomas (DB); Schmitt, Armin (DB)

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## ORIGIN

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 VERSION CS038316.1  
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 ORGANISM  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.  
 REFERENCE  
 1 Francis-Lang, H., Winter, C.G., Ventura, R.B., Björke, L.M.,  
 Lickteig, K., Adamkewicz, J.I., Zhang, H., and Hal, B.  
 Modulates as modifiers of the beta-catenin pathway and methods of use  
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 JOURNAL  
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 Best Local Similarity: 99.84 Mismatches: 1  
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RESULT 9					
CQ490536					
LOCUS	CQ490536	4515 bp	DNA	linear	PAT 30-JAN-2004
DEFINITION	Sequence 22403 from Patent WO0160860.				
ACCESSION	CQ490536				
VERSION	CQ490536.1	GI:41456155			

SOURCE ORGANISM	Homo sapiens (human)
Homo sapiens	

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

REFERENCE	AUTHORS	TITLE
1	Schlegel, R., Endege, W.O. and Monahan, J.E.	Genes differentially expressed in human prostate cancer and their

use  
Patent: WO 0160860-A 22403 23-AUG-2001;  
JOURNAL Millennium Predictive Medicine, Inc. (US)

FEATURES	location/Qualifiers
source	1. .4515
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Length:	4515

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Percent Similarity:	99.8%	Conservative:	0
Best Local Similarity:	99.8%	Mismatches:	1

Query Match:	99.7%	Indels:	1
DB:	6	Gaps:	0

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US-09-976-858-42 (1-1325) x CQ490536 (1-4515)

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159 CGCGTGTCTTCTGCTGCTCAATCCCTGTTTAAATGCGCCATTAACGGAGATTACG 218  
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Dd		399	ATTAGAAGAAATGCCAAGTATATCACGCCCATATTTTGGAAAAATTAATTAATTTT	458
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Dd		459	GAAATTTATGTATCCCAATGAGATTCTGTGGCTTTGAACACAGGTCACGCTTAGCAGG	518
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Dd		579	TGTGCTGGAGATGAGGTTACGAGTAGCCATGTGCATATGATTTATCGGAAGCACTTCGT	638
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Dd		639	CTTGATGACATAGGCGCATAGGGGAACAACAACAGCGCAGATAGTCAATCTGCTCTCCAT	698
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QY 361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380

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1299 CAGCTGCCGTCAATGGTAAAAAAGATGGTGATGTCAGAGATTACTGCTTTTGGGAT 1358

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441 LeuAlaValAlaGlyProValAlaGlyLysSerSerLeuSerAlaValLeuGly 460

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Qy 601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGlnPhe 620  
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 VERSION CQ492310.1 GI:41457929  
 KEYWORDS  
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 ORGANISM Homo sapiens  
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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.

REFERENCE  
 1 Schlegel, R., Endege, W.O. and Monahan, J.B.  
 Genes differentially expressed in human prostate cancer and their  
 use

JOURNAL Patent: WO 0160860-A 24177 23-AUG-2001;  
 Millennium Predictive Medicine, Inc. (US)  
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US-09-976-858-42 (1-1325) x CQ492310 (1-4515)

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DB 159 CGCGTTCCTTGCTGCTCAATCCCTTTTAAATGGCCATTAACGAGATTAGAG 218  
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 REFERENCE  
 1 Schlegel, R., Endege, W.O. and Monahan, J.E.  
 Genes differentially expressed in human prostate cancer and their  
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 REFERENCE  
 AUTHORS Schlegel, R., Endege, W.O. and Monahan, J.E.  
 TITLE Genes differentially expressed in human prostate cancer and their  
 use  
 JOURNAL Patent: WO 0160860-A 26500 23-AUG-2001;  
 Millennium Predictive Medicine, Inc. (US)

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 REFERENCE  
 1 Schlegel R., Endege W.O. and Monahan J.B.  
 Genes differentially expressed in human prostate cancer and their  
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 JOURNAL Patent: WO 0160860-A 28237 23-AUG-2001;  
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 Db 1479 GAATGGCCCCCAAGTCAACGGGCTGTGACGCTGCATGCAAGAAATGCTTATGTCTCAG 1538  
 QY 481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLySLeuYrGlu 500  
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 QY 521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLyS 540  
 Db 1659 GAGGATGTGATCTGACTGTGATGAGAGATCGGGGAAACACGCTGAGTGGAGGGCAGAAA 1718  
 QY 541 AlaArgValAsnLeuAlaArgAlaValYrGlnAspAlaAspIleYrIleuLeuAspAsp 560  
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 Db 1779 CCTCTCAGTGCAGTAAATGCGGAAAGTTTACAGACACTTGTGGAATGTGATTTGTCTCA 1838  
 QY 581 IleLeuHisGluLySLeuThrIleLeuValThrHisGlnLeuGlnYrLeuLysAlaIle 600

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 QY 621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLySAspAsnGlnGlnSerGlnGln 640  
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 QY 821 IleLeuAsnArgPheSerLySAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840  
 Db 2559 ATTTTAAATCGTTTCTCAAGACATGTGACACTTGAATGATTTCTGCGCTGACGTTT 2618  
 QY 841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValAlaSerValAlaValAlaVal 860  
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 Db 2679 ATTCCTTGATTCGCAATACCTTGTGTCCCTGTGAATCAATTTTCAATTTTCTTGGCGCA 2738  
 QY 881 TyrPheLeuGluThrSerArgAspValLysArgLeuGlnGlnSerThrThrArgSerProVal 900  
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 QY 921 GluArgYrGlnGlnLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLe 940  
 Db 2859 GAGAGGTTCAGGAACCTGTTGATGACACAGCAGGATTTTACATTCAGAGGCTTGTCTT 2918  
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## Alignment Scores:

Pred. No.: 0 Length: 5759  
 Score: 6766.00 Matches: 1321  
 Percent Similarity: 99.8% Conservative: 2  
 Best Local Similarity: 99.7% Mismatches: 0  
 Query Match: 99.7% Indels: 0  
 DB: 8 Gaps: 0

US-09-976-858-42 (1-1325) x AY081219 (1-5759)

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 QY 21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGln 40  
 Db 82 CGCGCTCTTCTGTGGGTCTCAATCCCTTGTTAAATGGCCATPAAACGAGATTAGAG 141  
 QY 41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGlnGluLeu 60  
 Db 142 GAAGATGATATGTAATTCAGTGTGCGCAGAAAGCCGCTCACAGCACTTGAGAGAGTTG 201  
 QY 61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80  
 Db 202 CAGGGGTCTGGGATTAAGAGATTTTAAGAGCTGAGAAATGACGCACAGAAAGCCCTCTT 261  
 QY 81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyLysPheThrLeu 100  
 Db 262 ACAGAGCATCTATAAGTGTACTGTGAATCTTATTTAGTTTGGGAATTTTACGTTA 321  
 QY 101 IleGlnLysSerAlaLysValIleGlnProIlePheLeuGlyLysIleLeuAsnTyrPhe 120  
 Db 322 ATTTGAGAAAGGCCAAAGTAAATCCAGCCATATTTTGGGAAAATTTATTAATTAATTT 381  
 QY 121 GluAsnTyrAspProMetCysSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140  
 Db 382 GAAATTAATGATCCCATGGAATTCGTGGCTTTGAACAGCCGTACCCCTATGCCAGCGTG 441  
 QY 141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisIleLeuTyrPheTyrHisValGln 160  
 Db 442 CTGACTTTTGGACGCTCATTTTGGCTATACGATCACTTATATTTTATACGTTGAG 501  
 QY 161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180  
 Db 502 TGTGCTGGGATGAGGTTTACAGATGACATGTGCCATATGATTTATGGAAGCACTTCGT 561  
 QY 181 LeuSerAspMetAlaMetGlyLysThrTrpThrGlnIleValAsnLeuSerAsn 200  
 Db 562 CTTAGTAACATGGCCATGGGAGAACACACAGCCAGATGATCATCTGCTGTCCAT 621  
 QY 201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220  
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QY 321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340  
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 Db 1342 TTAGCTGTGTGCGCCCGTGGGACAGGAAATCATCATCTGTAAATGCCGCTCGCGG 1401  
 QY 461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrAlaSerGln 480  
 Db 1402 GAATTTGGCCCAAGTACCGGCTGTGCAGCGTGAAGAAATGCTCATGTGCTCAG 1461  
 QY 481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGln 500  
 Db 1462 CAGCCTGGGTGTTCTCGGAATCTGAGAGTATATTTATTTGGGAAAGAAATACGA 1521  
 QY 501 LysGluArgTyrGlnLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520  
 Db 1522 AAGAACCATATGAAGAAAGTCAATAAGGCTGTGCTGCAAAAAGATTTACAGCGTTG 1581  
 QY 521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540  
 Db 1582 GAGGATGTGATCTACCTGTGTAGAGATTCGGGAAACCACTGATGAGAGGCGAGAA 1641  
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 Db 1642 GCAAGGATRAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCGAGCAT 1701  
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## RESULT 15

AR278592

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 6082)  
 Xu J., Dillon D.C., Mitcham J.L., Harlocker S.L., Jiang Y.,  
 Kalos M.D., Fanger G.R., Retter M.W., Stolk J.A., Day C.H.,  
 Vedrick T.S., Carter D., Li S.X., Wang A., Skeiky Y.A.W.,

6082 bp DNA linear PAT 10-APR-2003

TITLE Hepler, W.T. and Henderson, R.A.  
Compositions and methods for the therapy and diagnosis of prostate cancer

JOURNAL Patent: US 6512094-A 535 28-JAN-2003;

Corixa Corporation; Seattle, WA

FEATURES Location/Qualifiers

1..6082

/organism="unknown"

/mol\_type="genomic DNA"

ORIGIN

Alignment Scores:

Pred. No.: 0 Length: 6082

Score: 6760.00 Matches: 1324

Percent Similarity: 99.9% Conservative: 0

Best Local Similarity: 99.9% Mismatches: 1

Query Match: 99.6% Indels: 1

DB: 6 Gaps: 0

US-09-976-858-42 (1-1325) x AR278592 (1-6082)

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QY 21 ArgValPhePheTrpLeuAsnProLeuPheLysIleGlyHisIleArgArgLeuGlu 40  
DB 246 CCGGTCTTCTCGGTGGCTCAATCCCTGTTTAAATGGCCATTAACGAGATTAGAG 305  
QY 41 GluAspAspMetLysSerValLeuProGluAspAspSerGlnHisLeuGlyGluLeu 60  
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QY 241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260  
DB 906 ATGCAAGTTCTAATCAATCTCCGCGCTTGCAAAAGCTGTTTGGGAAGTTGTTCTATCA 965

QY 261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280  
DB 966 CTGAGAGATTAATAACGCAACTTTTCAACGATGCGACGATCAGAGCATGAAATGAATGTATA 1025  
QY 281 ThrGlyIleArgIleIleLysMetTrpAlaTrpGlyLysSerPheSerAsnLeuIleThr 300  
DB 1026 ACTGATTAAGATATATTAATAATGTACCGCTGGGAAAGTCAATTTCAATTTTATACC 1085  
QY 301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320  
DB 1086 AATTGGAAGAAGAGAGATTTCCAAAGATTCTGAGAAATGCTTGCTGCTGAGGGGATGAT 1145  
QY 321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrTrpVal 340  
DB 1146 TTGGCTGTGTTTTCAGTGCAAGCAAAATCAATCGTTTGGACCTTCAACCTACAGTG 1205  
QY 341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTrpGlyAla 360  
DB 1206 CTCTCGGCGAGTATACACGCGCGGTGTGTGGAGTACCGCTGTATGGGCT 1265  
QY 361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGlyArgValSerGluAlaIle 380  
DB 1266 GTGGCGGTGACCGTTACCTCTTCTCCCTAGCCATTGAGAGGGGTGACAGGCAATC 1325  
QY 381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400  
DB 1326 GTCAACATCCGAAGATCCAGACTTTTGTCTACTGTATGAGATATCACAGCGCAACGT 1385  
QY 401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420  
DB 1386 CAGCTGCGTCAGATGTAAAGATGGTGCATGTGCAGAGATTACGTCTTTTGGGAT 1445  
QY 421 LysAlaSerGluThrProThrLeuGlnLysLeuSerPheThrValArgProGlyGluLeu 440  
DB 1446 AAGCATCAGAGACCCCAACTATACAGGCCCTTCTTACTGTCAGACCTGGCAATTG 1505  
QY 441 LeuAlaValAlaGlyProValGlyValAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460  
DB 1506 TTAGCTGTGTGTGGCCCGCTGGAGCAGGGAATCATCATCTGTAAATGTGCCGTGGG 1565  
QY 461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTrpValSerGln 480  
DB 1566 GAATTGGCCCCAAGTACAGGCTGTACAGCGTGCATGGAAGATGGCTATGTGTCTCAG 1625  
QY 481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTrpGlu 500  
DB 1626 CAGCCCTGGGTGTCTCGGAACTGTGAGAGTAAATTTTATTTGGGAAGAAATACGA 1685  
QY 501 LysGluArgTrpGlyLysValIleLysValaCysAlaLeuLysLysAspLeuGlnLeuLeu 520  
DB 1686 AAGGAACGATATGAATAAGTCAATAAGGCTTGTCTGAAATAAGATTTTACAGCTGTG 1745  
QY 521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540  
DB 1746 GAGAGTGTGATCTGACTGTGATAGAGATCGGGAAACCACTGATGTGAGGGGAGANA 1805  
QY 541 AlaArgValAsnLeuAlaArgAlaValTrpGlnAspAlaAspIleTrpLeuLeuAspAsp 560  
DB 1806 GCAAGCGTAAACCTTGCAAGAGACAGATGATCAAGATGCTGACATGATCTCTGAGCAT 1865  
QY 561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCySerGln 580  
DB 1866 CCTCTCAGTGCAGTATGATCGGAAAGTTCGACACACTTGTGTGAACCTGTGTATTTGTC 1925  
QY 581 IleLeuHisGlyLysLysIleThrIleLeuValThrHisGlnLeuGlnTrpLeuLysAla 600  
DB 1926 ATTTTGCATGAAGAATCAAAATTTAGTCAATCAATGATCAAGTCTCAAGCTGCA 1985  
QY 601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTrpThrGluPhe 620  
DB 1986 AGTCAGATTCTGATATTTGAAGATGTAAATATGCTGCAGAAAGGAGCTTACACTAGTTC 2045  
QY 621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGlnSerGluGln 640



Db 2046 CTAATATCGTATGATTTGGCTCCCTTTAAAGAGATATAGAGAAAGTGAACA 2105  
 Qy 641 ProProValProGlyThrProThrLeuValGlnValGlnPheSerGluSerSerValTyr 660  
 Db 2106 CCTCAAGTTCAGGAATCCCACTCAAGAGATCGTACCTTCTCAGAGCTTCGGTTGG 2165  
 Qy 661 SerGlnGlnSerSerArgProSerLeuValAspGlyAlaLeuGluSerGlnAspThrGlu 680  
 Db 2166 TCTCAACAATCTTCTAGACCTCTTGAAAGATGGTCTCTGAGAGCCCAAGATACAGAG 2225  
 Qy 681 AsnValProValThrLeuSerGlnGlnAsnArgSerGlnGlyValGlyValGlyPheGlnAla 700  
 Db 2226 AATGCTCCAGTATCACTATCAAGAGAGAACCGTTCTGAAGAGAAAGTTGTTTCAAGGCC 2285  
 Qy 701 TyrLeuAsnThrPheArgAlaGlyAlaHisTyrPileValPheLeuPheLeuLeuLeu 720  
 Db 2286 TATAAGAAATTCCTCAGAGCTGGTCTCACTGGAATTCCTCATTTTCTTATTTCTCTCA 2345  
 Qy 721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTyrPheLeuSerTyrThrAlaAsn 740  
 Db 2346 AACCTGACGCTCAGGTTGGCTTATGCTTCAAGATGGTGGCTTTCATACCTGGGCAAC 2405  
 Qy 741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760  
 Db 2406 AAACAAGATCTAAATGCTCACTGTAATGAGAGAGAAATGTAACCGAGAGCTAGAT 2465  
 Qy 761 LeuAsnTyrTyrLeuGlyLysTyrSerGlyLeuThrValAlaThrValLeuPheGlyLys 780  
 Db 2466 CTTAATCTGATCTTGGAAATTTATTCAGGTTTAACTGTAACGCTTCTTTTGGCAATA 2525  
 Qy 781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800  
 Db 2526 GCAAAATCTCAATGATATCTAAGCTCTGTTAACTCTTCACAAACTTTGACAAACAA 2585  
 Qy 801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820  
 Db 2586 ATGTTTGAATCAATCTGAAGCTCCGGATTAATCTTTGATAGAAATCCATAGAGAGA 2645  
 Qy 821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840  
 Db 2646 ATTTTAAATCGTTTCTCCAAAGACATTTGACACTTGATGATTTGCTGCGCTGACGTT 2705  
 Qy 841 LeuAspPheIleGlnThrLeuGlnGlnValGlyValValSerValAlaValAlaVal 860  
 Db 2706 TTAGATTCATCAAGACATTTGCTACAGAGTGGTGGTCTCTGCTGCTGCTGCTGCTG 2765  
 Qy 861 IleProTyrPileAlaIleProLeuValProLeuGlyLysIlePheIlePheLeuArgArg 880  
 Db 2766 ATTCCTTGATCGCAATACCTTGGTTCCTCCCTTGGAAATCATTTTCTTGGCGCA 2825  
 Qy 881 TyrPheLeuGlnThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900  
 Db 2826 TATTTTGGAAACGTCAGAGATGAGAGCGCTCGAATCTACAACTCGAGTCCAGTG 2885  
 Qy 901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTyrPheIleArgAlaTyrTyrValGly 920  
 Db 2886 TTTTCCCACTTCATCTTCTCCAGGGGCTCTGACATCCGGGCAATACAGAGAGAA 2945  
 Qy 921 GlnArgCysGlnGlnLeuPheAspAlaHisGlnAspLeuHisSerGlnAlaTyrPheLeu 940  
 Db 2946 GAGAGGTGTCAGGAATCTTTGATGACACAGAGATTTACATTCAGAGCTTGGTTCTTG 3005  
 Qy 941 PheLeuThrThrSerArgTyrPheAlaValAlaArgLeuAspAlaIleCysAlaMetPheVal 960  
 Db 3006 TTTTGGACAAAGCTCCGCTGGTGGCTGCTGCTGATGATGATGATGATGATGATGATG 3065  
 Qy 961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyValGlnValGly 980  
 Db 3066 ATCATCGTGGCTTGGGCTCCGATTCGGCAAAACCTGAGATGCCGGGCAAGGTGGT 3125  
 Qy 981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTyrCysValArgGlnSer 1000

Db 3126 TTGGCACTGCTCATGACCTCAAGCTCATGGGAGATTTTCAGTGGTGTTCGACAAAGT 3185  
 Qy 1001 AlaGlnValGlnAsnMetMetIleSerValGlnArgValIleGlnTyrThrAspLeuGln 1020  
 Db 3186 GCTGAAGTTGGAAT 3245  
 Qy 1021 LysGlnAlaProTyrGlnTyrGlnLysArgProProAlaTyrProHisGlnGlyVal 1040  
 Db 3246 AAAGAGACCTTGGGAATATCAAGAAACGCCACCAAGCTGGCCCCCATGAAGAGTG 3305  
 Qy 1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060  
 Db 3306 ATATCTTTGACAAATGTGAATCTTCACTGATGACAGTCCAGCTGGGCTCTCTGATCAAGCAT 3365  
 Qy 1061 LeuThrAlaLeuIleLysSerGlnGlnLysValGlyIleValGlyArgThrGlyValGly 1080  
 Db 3366 CTGACAGACCTATTAAATCAAGAAAGAGTGGCATTTGGAGAAAGAACCGAGACTGGA 3425  
 Qy 1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGlnGlyLysIleTyrPile 1100  
 Db 3426 AAAAGTCCCTCATCTCAGCCCTTTTATGATTTGTCAGAACCCGAAAGTAAATTTGGATT 3485  
 Qy 1101 AspLysIleLeuThrThrGlnIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120  
 Db 3486 GATAAGATCTTGACAACTGAATTTGCACTTCAAGATTTAAAGAGAAATATGCAATCATTA 3545  
 Qy 1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGln 1140  
 Db 3546 CCTCAGGAACCTGTTTGTTCATCTGGAAACAATGAGAAACCTGGAATCCCTTATATGAG 3605  
 Qy 1141 HisThrAspGlnGlnLeuTyrAsnAlaLeuGlnGlnValGlnLeuLysGlnThrIleGln 1160  
 Db 3606 CACAGAGTGAAGAACTGTGAATCTTCAAGAGGTGACAACTTAAAGAAACCTTGA 3665  
 Qy 1161 AspLeuProGlyLysMetAspThrGlnLeuAlaGlnSerGlySerAsnPheSerValGly 1180  
 Db 3666 GATCTTCTCGTGAATAATGATATGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 3725  
 Qy 1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuAlaGlyLysAsnGlnIleLeuIleIle 1200  
 Db 3726 CAAGACAACTGGTGTGCTTCCAGGGCAATTTCCAGAAACCAATATATGATTTAT 3785  
 Qy 1201 AspGlnAlaThrAlaAsnValAspProArgThrAspGlnLeuIleGlnLysLysIleArg 1220  
 Db 3786 GATGAAGACGCGCAATGTGATTCAGAACTGATGATTAATCAAAAAAAC -CG 3844  
 Qy 1221 GlnLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240  
 Db 3845 GAGAAATTTGGCCACTGACCGGTGCTTACATTTGACACAGATTTGAACCATTTATGAC 3904  
 Qy 1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGlnTyrAspGluProTyrVal 1260  
 Db 3905 AGCGACAAAGATATGTTTATGATTCAGAAAGACTGAAAGATATGAGAGCGATATGT 3964  
 Qy 1261 LeuLeuGlnAsnLysGlnSerLeuPheTyrLysMetValGlnGlnLeuGlyLysValGln 1280  
 Db 3965 TTGCTGCAAAATTAAGAGAGCTTATTTACAGATGTGTGACAACTGGGCAAGCAGAA 4024  
 Qy 1281 AlaAlaAlaLeuThrGlnThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300  
 Db 4025 GCCCGTGCCTCATCGAAACGCAAAACAGGATATCTTCAAAAGAAATTAATCAATATT 4084  
 Qy 1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320  
 Db 4085 GGTCACTGACCAACATGTTTAAACAACCTTCAATGACAGAGCCCTCAACCTTAATATT 4144  
 Qy 1321 PheGlnThrAlaLeu 1325  
 Db 4145 TTGAGACAGCACTG 4159



GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 14, 2006, 07:38:05 ; Search time 1691 Seconds  
(without alignments)  
5222.187 Million cell updates/sec

Title: US-09-976-858-42

Perfect score: 6787  
Sequence: 1 MLPVYQEKRPPLDANLCS.....MTWTSNQSPSTLTFETAL 1325

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ \_p2n.model -DEV=xlh  
-O=/abs/ABSSWB/epool/US0976858/runat 13032006.170057.11733/app.query.fasta.1  
-DB=N Geneseg -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=biolum62 -TRANS=human40.cdi -LIST=45  
-DOCLALIGN=200 -THR SCORE=Pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTMT=Pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=AB808  
-USER=US0976858 @CGN 1.1.727 @runat 13032006.170057.11733 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N\_Geneseg\_21.\*

1: geneseqn1980s:\*  
2: geneseqn1908s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6787	100.0	3978	6	ABK92135
2	6787	100.0	3978	11	ADN39251
3	6785	99.9	5271	12	ADH10611
4	6785	99.9	5284	12	ADH10612

5	6785	99.9	5833	12	ADH10624	Adh10624 Human can
6	6785	99.9	5862	12	ADH10626	Adh10626 Human can
7	6781	99.9	4078	14	ADM14765	Adm14765 Tumour-ass
8	6779	99.9	4231	2	AA230078	AA230078 CDNA enco
9	6779	99.9	4231	5	AAH81778	AAH81778 Human dif
10	6779	99.9	4231	8	ABV75072	ABV75072 Human Dev
11	6779	99.9	4231	11	ADN39253	Adn39253 Cancer/an
12	6779	99.9	4231	14	ACL38944	ACL38944 ABCC4 cod
13	6779	99.9	4231	14	AEA00097	Aea00097 Human TAT
14	6779	99.9	4231	14	AEA00617	Aea00617 Human TAT
15	6779	99.9	4231	13	ADR66822	Adr66822 Human pro
16	6779	99.9	5832	13	ADR65919	Adr65919 Human pro
17	6779	99.9	5870	10	ADB75177	Adb75177 Prostate
18	6779	99.9	5871	14	ADX98506	Adx98506 Human ATP
19	6779	99.9	5871	14	ADZ49388	Adz49388 Insulin s
20	6770	99.7	4515	5	ABV24188	ABV24188 Human pro
21	6770	99.7	4515	5	ABV26511	ABV26511 Human pro
22	6770	99.7	4515	5	ABV20669	ABV20669 Human pro
23	6770	99.7	4515	5	ABV22410	ABV22410 Human pro
24	6770	99.7	4515	5	ABV24580	ABV24580 Human pro
25	6770	99.7	4515	5	ABV28224	ABV28224 Human pro
26	6760	99.6	6082	4	AAH93828	AAH93828 Human pro
27	6760	99.6	6082	4	AAH85142	AAH85142 Human pro
28	6760	99.6	6082	4	AAH85142	AAH85142 Human pro
29	6760	99.6	6082	5	ACA59729	ACA59729 Prostate
30	6760	99.6	6082	6	ABL95292	Abi95292 Human P51
31	6760	99.6	6082	8	ACC95456	Acc95456 Prostate
32	6760	99.6	6082	10	ADB13985	Adb13985 Human pro
33	6760	99.6	6082	10	ADG26401	Adg26401 Human pro
34	6647	97.9	3913	12	ADQ59423	Adq59423 Human can
35	6600.5	97.3	6140	4	AAH93829	AAH93829 Human pro
36	6600.5	97.3	6140	4	AAH85143	AAH85143 Human pro
37	6600.5	97.3	6140	4	AAH85143	AAH85143 Human pro
38	6600.5	97.3	6140	5	ACAS9730	Acas9730 Prostate
39	6600.5	97.3	6140	6	ABL95293	Abi95293 Human P51
40	6600.5	97.3	6140	8	ACC95457	Acc95457 Prostate
41	6600.5	97.3	6140	10	ADB13986	Adb13986 Human pro
42	6600.5	97.3	6140	10	ADG26402	Adg26402 Human pro
43	6357	93.7	4395	10	ACC95747	Acc95747 Prostate
44	6357	93.7	4395	8	ADB14457	Adb14457 Expressio
45	6357	93.7	4395	10	ADG26980	Adg26980 Human pro

#### ALIGNMENTS

RESULT 1  
ABK92135  
ID ABK92135 standard; DNA; 3978 BP.  
AC ABK92135;  
DT 15-AUG-2002 (first entry)  
DE Prostate cancer-associated DNA sequence #21.  
KM Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;  
KW gene therapy; gene; ds.  
OS Mammalia.  
XX  
XX WO200230268-A2.  
XX  
XX 18-APR-2002.  
XX  
XX  
XX 12-OCT-2001; 2001WO-US032045.  
XX  
XX 13-OCT-2000; 2000US-00687576.  
XX 08-DEC-2000; 2000US-00733288.  
XX 08-DEC-2000; 2000US-00733742.  
XX 24-JAN-2001; 2001US-0263957P.  
XX 16-MAR-2001; 2001US-0276791P.  
XX 16-MAR-2001; 2001US-0276888P.  
XX 06-APR-2001; 2001US-0281922P.



QY 501 LysGIuArgTyrGluValIleuValaCysAlaLeuLysLysAspLeuGlnLeu 520  
Db 1501 AAGGAACATATGAAAAAGCTATAAAGGCTGTGCTGAAAAAAGATTTCAGCTGTG 1560  
QY 521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540  
Db 1561 GAGAGTGTGATCTGATCTGTATAGAGATCGGGAAACACCTGATGAGGGAGAA 1620  
QY 541 AlaArgValAsnLeuLysArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAsp 560  
Db 1621 GCACGGGTAACCTTGCAGAGAGAGCTGTATCAAGATGCTGACATCTATCTCTGGAGCAT 1680  
QY 561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGlnLeuGlyLeuGln 580  
Db 1681 CCTCAGATGAGATGAGATGCGGAAGTATGACAGACCTGTGTGAACTGTATTTGTCAA 1740  
QY 581 IleLeuHisGluValIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600  
Db 1741 ATTTTGATGAGAGATCAATTTTATGACTCATGAGTCACTGAGTACTCAAGCTGCA 1800  
QY 601 SerGlnIleLeuLysLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGlnPhe 620  
Db 1801 AGTCAGATTCTGATATTGAAAGATGTTAAATGTCGAGAGAGGAGCTTACCTGAGTTC 1860  
QY 621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGlnGlnSerGlnGln 640  
Db 1861 CTAAATATGATATGATTTGGCTCCCTTTTAAAGAAAGATTAAGAGAAAGTAAACA 1920  
QY 641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGlnSerSerValTyr 660  
Db 1921 CCTCAGTTCAGAGAACTCCACACTTAAGAAATGATCTTCTGAGATCTTCGGTTGG 1980  
QY 661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGlnSerGlnAspThrGln 680  
Db 1981 TCTCAACATCTTCTAGACCCCTCTTGAAGATGTCCTGAGAGCAGCAAGATACAGAG 2040  
QY 681 AsnValProValThrLeuSerGlnGlnAsnArgSerGlnGlyLysValGlyPheGlnAla 700  
Db 2041 AATGCCCACTATCACTATCAGAGAGAAACCGTTCTGAAGGAAAGTTGGTTTCAGGCC 2100  
QY 701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrrIleValPheIlePheLeuIleLeuLeu 720  
Db 2101 TATTAAGATTACTTCAGAGCTGTGCTCTCATGATTTCTTCTTATTTCTCTTA 2160  
QY 721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrrPheLeuSerTyrTrrAlaAsn 740  
Db 2161 AACACTGACGTCAGGTTGCTATGCTTCAAGATTGGTGGCTTTCATACCTGGCAAC 2220  
QY 741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGlnLysLeuAsp 760  
Db 2221 AAACCAACATATGCTAAATGCTCATCTAAATGAGAGAGAAATGTAAACCGAGAAAGCTAAT 2280  
QY 761 LeuAsnTrrPyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780  
Db 2281 CTTAATCTGACTTACGAATTTATTCAGGTTTAACTGATGCTAACCGTCTTTTGTGCAATA 2340  
QY 781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800  
Db 2341 GCAAAATCTCTATGTAATTCAGTTCCTGTTAACTCTTCACAAACCTTGCACAAACAA 2400  
QY 801 MetPheGlnSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820  
Db 2401 ATGTTTGGATCAATCTGAAAGCTCCGGTATTAATCTTGTATGAAATCCATATAGAAAGA 2460  
QY 821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840  
Db 2461 ATTTTAAATCGTTTCTCCAAAGACATTGGACCTTGGATGATTTGCTGCGCTGACGTTT 2520  
QY 841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860  
Db 2521 TTAGATTTCATCCAGACATTCCTACAGATGTTGGTGATGCTCTGTGCTGTGCGCGG 2580

QY 861 IleProTrrIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuAspArg 880  
Db 2581 ATTCCTTGATCGGAATACCTTGTTCCCTTGGAATCATTTTCTTCGGGCA 2640  
QY 881 TyrPheLeuGlnThrSerArgAspValLysArgLeuGlnSerThrThrArgSerProVal 900  
Db 2641 TATTTTGGAAAGTCAGAGATGTGAAGGCTCGGAATCTCAATCCGAGATCCAGTG 2700  
QY 901 PheSerHisLeuSerSerSerLeuGlnGlyLeuThrThrIleArgAlaTyrLysAlaGlu 920  
Db 2701 TTTTCCACTGTATCTTCTCTCAGGGGCTCTGACCATCCGGGCAATACAGAAAGCGAA 2760  
QY 921 GluArgCysGlnGlnLeuPheAspAlaHisGlnAspLeuHisSerGlnAlaTrrPheLeu 940  
Db 2761 GAGAGTGTCAAGAACTGTTGATGCACACAGAAATTTACATTCAGAGCTTGGTTCTG 2820  
QY 941 PheLeuThrThrSerArgTrrPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960  
Db 2821 TTTTGAACAAGTCCCGCTGGTTCCCGTCCGTCTGATGTCATGTCATGTCATGTTGTC 2880  
QY 961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980  
Db 2881 ATCATCGTTGCTTTGGGTCCCTGATTCGCAAAAACCTGATGTCGGGACAGTGGT 2940  
QY 981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrrCysValArgGlnSer 1000  
Db 2941 TTGGACTGTCTATGCCCTCACCTCATGGGAGTGTTCAGTGTGTGTTCCAGAAAT 3000  
QY 1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGln 1020  
Db 3001 GCTGAAGTTGGAATATGATGATCTCAGTAAAGGGGCATGTAATACACAGACTTGA 3060  
QY 1021 LysGluAlaProTrrGluTyrGlnLysArgProProAlaTrrProHisGluGlyVal 1040  
Db 3061 AAAGAGCACTTGGGAATATCAGAAACGCCACACACGCTGGCCCCAGAAAGAGATG 3120  
QY 1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060  
Db 3121 ATTAATCTTGCAATGTGAATTTCACTGATCAAGTGGGCTCTGTGATCTGAAGAT 3180  
QY 1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080  
Db 3181 CTGACAGCACTTAATATATCAAGAAAGGTTGGCATTTGGGAAAGACCGAGCTGGA 3240  
QY 1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGlnGlyLysIleTrrIle 1100  
Db 3241 AAAAGTCCCTCATCTCAGCCCTTTTATGATTTGCAGAACCCGAAAGTTGAAT 3300  
QY 1101 AspLysIleLeuThrThrGlnIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120  
Db 3301 GATTAAGATCTTGACAACTGAATTTGACTTACAGATTTTAAGAAAGAAATGTCAATCA 3360  
QY 1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGln 1140  
Db 3361 CCTCAGAAACCTGTTTGTTCATCTGAAACATTAAGAAACCTGGAATCCCTTAATAG 3420  
QY 1141 HisThrAspGlnGluLeuTrrPheAlaLeuGlnGlnValGlnLeuLysGlnThrIleGlu 1160  
Db 3421 CACACGATGAGGAACGTGGAAATGCTTAAACAGAGTAACAATTAAGAAACCAATGAA 3480  
QY 1161 AspLeuProGlyLysMetAspThrGlnLeuAlaGlnSerGlyLysAsnAspPheSerValGly 1180  
Db 3481 GATCTCTCGGTAAAGATGATACGATTTAGCAAGATTAAGATCCAAATTTAGTGTGA 3540  
QY 1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200  
Db 3541 CAAGAGCAACGTGGTGGCTTCCAGGGCAATTCAGGAAATAACGATATTTGATTTAT 3600  
QY 1201 AspGluAlaThrAlaAsnValAspProArgThrAspGlnLeuIleGlnLysLysIleArg 1220  
Db 3601 GATGAAGCGAGCGGCAATGTGATCCAAAGCATATGATGTTAAATACAAAAAATCCGG 3660  
QY 1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240

DB 3661 GAGAAATTTGCCCATGACCCCTGCTAACCATTTGACACAGATTGACACCATTTATTGAC 3720  
QY 1241 SerrapylisileMeValleuaspsergylargleuyltyrAspGluProTyrVal 1260  
DB 3721 ACCGCAAGATATAGTTTATGATTCAGAGACATGAAAGATATGATGACCGTATGTT 3780  
QY 1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280  
DB 3781 TTGCTGCAAAATTAAGAGAGCCTATTTTTCAAGATGCTCAACATGGGCAAGCAGAA 3840  
QY 1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300  
DB 3841 GCCGCTGCCCTCAGTGAACAGCAAAACAGGTATCTTCMAAAGAAATTTATCCATATT 3900  
QY 1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyLysProSerThrLeuThrIle 1320  
DB 3901 GGTCACTGACCAACATGCTTTCAACACTTCCATTGACAGCCCTCCAGCTTAATCTATT 3960  
QY 1321 PheGluThrAlaLeu 1325  
DB 3961 TTCGAGACGACACTG 3975  
RESULT 2  
ADN39251  
ID ADN39251 standard; cDNA; 3978 BP.  
AC XX  
XX  
DT 17-JUN-2004 (first entry)  
DE XX  
XX  
KW Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:569.  
XX  
XX Human; differential expression; cancer; angiogenic disorder;  
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;  
KW inflammatory disease; autoimmune disease;  
KW retinal neovascularization syndrome; scarring; uterine fibroid;  
KW detection; diagnosis; prognosis; drug screening; drug targeting;  
KW wound healing; contraception; cytostatic; cardiac; immunomodulatory;  
KW vulnery; gene therapy; vaccine; gene; ss.  
XX  
XX Homo sapiens.  
OS  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
XX  
PF 13-NOV-2002; 2002WO-US036810.  
XX  
XX 13-NOV-2001; 2001US-0350666P.  
PR 21-NOV-2001; 2001US-0332464P.  
PR 29-NOV-2001; 2001US-0334393P.  
PR 03-DEC-2001; 2001US-0335394P.  
PR 14-DEC-2001; 2001US-0340376P.  
PR 08-JAN-2002; 2002US-0347211P.  
PR 10-JAN-2002; 2002US-0347349P.  
PR 08-FEB-2002; 2002US-0355250P.  
PR 13-FEB-2002; 2002US-0356714P.  
PR 20-FEB-2002; 2002US-0359077P.  
PR 29-MAR-2002; 2002US-0368609P.  
PR 04-APR-2002; 2002US-0370110P.  
PR 12-APR-2002; 2002US-0372246P.  
PR 05-JUN-2002; 2002US-0386614P.  
PR 16-JUL-2002; 2002US-0396839P.  
PR 22-JUL-2002; 2002US-0397775P.  
PR 22-JUL-2002; 2002US-0397845P.  
PR 09-SEP-2002; 2002US-0409450P.  
XX  
XX (EOSB-) EOS BIOTECHNOLOGY INC.  
PA  
PI Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Heverzi PA;  
PI Mack DH, Murray R, Watson SR, Willson KE, Zlotnick A;  
XX

DR WPI: 2003-468649/44.  
DR P-PSDB; ADN39252.  
XX  
XX Determining the presence or absence of a pathological cell in a patient,  
PT useful for diagnosing, prognosing or treating cancer, comprises detecting  
PT a nucleic acid in a biological sample.  
XX  
XX Claim 8; SEQ ID NO 569; 1385bp; English.  
PS  
XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064)  
CC whose expression is upregulated or downregulated in specific cancers or  
CC other diseases such as angiogenic or fibrotic disorders, and to methods  
CC of determining the presence or absence of a pathological cell in a  
CC patient by detecting a nucleic acid at least 80% identical to those of  
CC the invention or by detecting a polypeptide of the invention. The  
CC invention also relates to expression vectors and host cells comprising a  
CC nucleic acid of the invention; antibodies which specifically bind a  
CC polypeptide of the invention; use of such antibodies for drug targeting;  
CC and methods of screening for modulators of activity or expression of the  
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,  
CC antibodies and methods are useful for diagnosing, prognosing and treating  
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,  
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal  
CC neovascularization syndromes, scarring and uterine fibroids. They may  
CC also be useful in wound healing and in contraception. The present  
CC sequence represents a nucleic acid sequence of the invention.  
XX  
SQ Sequence 3978 BP; 1113 A; 817 C; 956 G; 1092 T; 0 U; 0 Other;  
XX  
Alignment Scores:  
Pred. No.: 0 Length: 3978  
Score: 6787.00 Matches: 1325  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 11 Gaps: 0  
US-09-976-858-42 (1-1325) x ADN39251 (1-3978)  
QY 1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAsnAlaAsnLysCysSer 20  
DB 1 ATGCTGCCCGCTGACAGAGAGTGAAGCCCAACCGCTGAGAGAGCGAAGCTGCTCA 60  
QY 21 ArgValPhePheTyrTyrLeuAsnProLeuPheLysIleGlyHisLysArgLysGlu 40  
DB 61 CGCGGTCTCTGCTGCTCAATCCCTGTTAAATGGCCATTAACGAGATTAG 120  
QY 41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLysGlyGlnLeu 60  
DB 121 GAAGATGATGATGATTCAGTCTGCCAGAGACCGCTCAAGACCTTGAGAGAGATTG 180  
QY 61 GlnGlyPheTyrPAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80  
DB 181 CAGAGTCTCGGATTAAGAAAGATTTAAGACGTAGAGATGACGACAGAGCTCTTTA 240  
QY 81 ThrArgAlaIleIleLysCysTyrTyrLysSerTyrLeuValLeuGlyIlePheThrLeu 100  
DB 241 ACAAGAGCATCATTAAGTTGTAACGAAATCTTATTTAGTTGGGAATTTTACGTTA 300  
QY 101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120  
DB 301 ATTGAGAAAGTCCAAAGTATCCAGCCCAATTTTGGGAAATTAATTATATT 360  
QY 121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaThrVal 140  
DB 361 GAAATTTATGATCCATGATTTCTGTGCTTTGAACAAGGCTAGCCGCGGTG 420  
QY 141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisIleLysTyrPheTyrHisValGln 160  
DB 421 CTGACTTTTGGACGCTCATTTTGGCTATGCTATGCACTATATTTTATCACCTTAG 480  
QY 161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180

481 TGTGCTGGGATGAGTTACGAGTACCATGTGCTCATATGATTTATCGAAGGCACTTGCT 540  
QY LeuSerAsnMetAlaMetGlyIleThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200  
DB 541 CTTAGTAACATGGCCATGGGAAAGACACACAGGCGCATAGTACATCTGTGCTGCAT 600  
QY AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuThrAlaGlyProLeu 220  
DB 601 GATGTGAACAACTTTGATCAGGTGACAGGTTCTTACACTTCTGTGGGACAGACACAG 660  
QY 221 GlnAlaIleValThrAlaLeuLeuThrMetGlyIleGlyIleSerCysLeuAlaGly 240  
DB 661 CAGGGGATCGCAGTGCCTGCTACTGAGATGAGATGAGAAATTCGGCTCTGGG 720  
QY 241 MetAlaValIleuIleIleLeuLeuProLeuGlnSerCysPheGlyIleLeuPheSerSer 260  
DB 721 ATGGAGATTCTAATCAATCTCTGCTGCCTGCAAGCTGTTTGGGAAGTGTTCATCA 780  
QY 261 LeuAspSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280  
DB 781 CTGAGAGAGTAACCTGCACACTTTCACGATGCCAGATGACAGATGACATGATTAATTA 840  
QY 281 ThrGlyIleArgIleIleLysMetIleAlaArgIleLysSerPheSerAsnLeuIleThr 300  
DB 841 ACTGGTATTAAGGATATAATAAATGATACGCTGGAAAGTCAATTTTCAAACTTATATAC 900  
QY 301 AsnLeuAlaGlyLysGlyGlyIleSerIleLeuAlaGlySerSerCysLeuAlaGlyMetAsn 320  
DB 901 AATTGAGAAAGAAAGAGATTTCCAAAGATTCGAGAAAGTTCTGCTCCAGGGGAGAT 960  
QY 321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrVal 340  
DB 961 TTGGCTTCTGTTTTCAGTGCACAGCAAAATCATCGTTTGTACACTTCCACCTACGCT 1020  
QY 341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuThrValAla 360  
DB 1021 CTCCCTCGGAGTGTATCAGCCAGCCGCTGTTCTGTGCGAGTACGCTGATGAGGCT 1080  
QY 361 ValAlaGlyLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380  
DB 1081 GTGCGGCTGACGGTTACCTCTTCTTCCCTCAGCATTTGAGAGGGGTGCAGAGCAATC 1140  
QY 381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGlyIleSerGlnArgAsnArg 400  
DB 1141 GTACAGATCCGAAAGATCCAGACCTTTTGTCTACTGATGAGATTCACAGGCGCAACCT 1200  
QY 401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheThrAsp 420  
DB 1201 CAGCTGCCGTGATGTGTAAAGATGGTGCATGTGCAGATTTTACTGCTTTTGGGAT 1260  
QY 421 LysAlaSerGluThrProThrIleuGlnGlyLeuSerPheThrValArgProGlyGlyLeu 440  
DB 1261 AAGGATCATGAAACCCCAACTCTACAGGCTTTCTTCACTGTACAGCTGCGCAATTC 1320  
QY 441 LeuAlaValAlaGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460  
DB 1321 TTAGCTGTGCTGCGCCCTGAGAGCAGGAAATCATCACTTTAAGTGCCTGCTCGGG 1380  
QY 461 GlnLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaIleValSerGln 480  
DB 1381 GAATTTGGCCCCCAAGTCAAGGCTGTGCTGAGCTGCAAGTGAATTTTATTTGGGAAGAAATACAA 1440  
QY 481 GlnProThrPheValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysArgIle 500  
DB 1441 CAGCCCTGGGTCTCTCGGAACTCTGAGAGATTAATTTATTTTGGGAAGAAATACAA 1500  
QY 501 LysGluArgIleArgIleValIleLysValCysAlaLeuLysLysAspLeuGlnLeuLeu 520  
DB 1501 AAGGAAACATATGAAAAAGTCTAAGAGCTTGTCTGTAAAAAGATTTTACAGCTGTTC 1560  
QY 521 GlnAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540  
DB 1561 GAGGATGTGATCTGACTGTGATGAGATCGGGAAACACGCTGATGTGAGAGGCAAGAA 1620

541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560  
QY 1621 GCAGGGTAAACCTTGCAAGGACAGTGTATCAAGATGCTGACATCTTCTGACCAT 1680  
DB 561 ProLeuSerAlaValAspAlaGlyValSerArgHisLeuPheGlyLeuCysIleCysGln 580  
QY 1681 CCTGTCAAGTGAAGTAAAGTGGGAAAGTTAGCAGACCTTGTTCGAACCTGTATTTGTCAA 1740  
DB 581 IleLeuHisGlyLysIleThrIleLeuValThrHisGlnLeuGlnThrThrLeuValAla 600  
QY 1741 AATTTCATGTGAAGATCACAAATTTAGTGTCTATCATCGTTGCAGTACCTCAAAAGCTCA 1800  
DB 601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGlyPhe 620  
QY 1801 AGTCAGATTCTGATTTGAAAGATGTGTAATGTGTGCAAGAGGGACTTACATCAGATTC 1860  
DB 621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGlnGlnSerGln 640  
QY 1861 CTAAATCTGGTATATGATTTTGGCTCTTTTAAAGAAAGATTAATGAGAAAGTGAACA 1920  
DB 641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGlySerSerValTyr 660  
QY 1921 CCTCCAGTTCAGGAACTCCACACTAAGGAAATGTACCTTCTCAGAGTCTTGGTTCG 1980  
DB 661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGlnSerGlnAspThrGlu 680  
QY 1981 TCTCAACATTTCTTACGCTCTCTGTAAGATGTGTCTGAGAGCCAAAGTACAGAG 2040  
DB 681 AsnValProValThrLeuSerGlnGluAsnArgSerGlnGlyLysValGlyPheGlnAla 700  
QY 2041 AATGTCCAGTTACATCATCAGAGAGAACCGTTCTGAAGAAAGTTGGTTTCAGGCC 2100  
DB 701 TyrLysAsnTyrPheArgAlaGlyAlaHisTyrIleValPheIlePheLeuIleLeuLeu 720  
QY 2101 TATTAAGATTTACTCAGAGCTGTGTCTCAGCTGAGATTCCTTCAATTTCTTATCTCTCA 2160  
DB 721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTyrThrLeuSerTyrThrAlaAsn 740  
QY 2161 AACACTGAGCTCAGGTGTGCTTATGTCTTAAGATGTGTGTCTTCAATCTGAGGCAATC 2220  
DB 741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyAlaAsnValThrGlyLysLeuAsp 760  
QY 2221 AAACAAAGTATGCTAAATGTACCTGTAAATGAGAGGAAATGTACCGGAAAGTATGAT 2280  
DB 761 LeuAsnTyrTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780  
QY 2281 CTTAACCTGTACTTACGAAATTTATTCAGTTTAACTGTACCTGCTCTTCTTGGCAT 2340  
DB 781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800  
QY 2341 GCAAGATCTCTAATGTGATTTTACGCTCTGTGTAACTTTTCAAACTTTGCACAAACAA 2400  
DB 801 MetPheGlnSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820  
QY 2401 ATGTTTGAATGATTTGAAAGCTCCGCTATTTATTTGTATGAATCCAAATGAGAAAG 2460  
DB 821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840  
QY 2461 AATTTAAATCGTTTCTCCAAAGACATTTGACACTTGTGATGATTTTGGCTGCGCTACGTTT 2520  
DB 841 LeuAspPheIleGlnThrLeuLeuGlnValAlaGlyValAlaValSerValAlaValAlaVal 860  
QY 2521 TTAGATTTTCAACAGACATTTGTAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2580  
DB 861 IleProThrIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880  
QY 2581 ATTCTTGATGATCGCAATACCTTGTTCCTTGTGATTCATTTTCTTCTGCGGGA 2640  
DB 881 TyrPheLeuGlnThrSerArgAspValLysArgLeuGlnSerThrThrArgSerProVal 900  
QY 2641 TATTTTGGAAACGTCAAGAGATGTGAAGGCTCGAATCTACACATCGGAGTCCAGTG 2700



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QY 901 PheSerHisLeuSerSerLeuGlnGluThrIleArgAlaTyrLysAlaGlu 920
DB 2701 TTTTCCCATCTTGTATCTTCTCCAGGGGCTCTGGACATCCGGGCATCAAGAGAGA 2760
QY 921 GluArgGlnGlnLeuPheAspAlaHisGlnAspLeuHisSerGluAlaTrpPheLeu 940
DB 2761 GAGAGGTGTCAGAACTGTTTATGTCACACAGGATTTACATTCAGAGGCTTGTTCTTG 2820
QY 941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
DB 2821 TTTTGGACACGTCCTGGCTGGTCCCTGCTCCCTGATGATCCATCTGTCCATGTTTGTG 2880
QY 961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
DB 2881 ATCATGTTGGCTTGGTGGTCCCTGATTTGGCAAAACTCTGGATGCCGGACAGGTGGT 2940
QY 981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
DB 2941 TTGGGACGTGCTATGCTCCCTCAGCTCATGGGATGTTTCAGTGTGTTGACAAAGT 3000
QY 1001 AlaGluValAlaGlnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020
DB 3001 GCTGAAGTTGAGAAATGATGATCTCAGTAGAAAGGATCATTAATGACACAGCTTGA 3060
QY 1021 LysGluAlaProTyrGluTyrGlnLysArgProProAlaTrpProHisGluVal 1040
DB 3061 AAAGAAAGCACCCTGGGATATATCAAGAAAGCCCAACCAAGCTGGCCCATGAAGAGTG 3120
QY 1041 IleIlePheAspAsnValAsnMetTyrSerProGlyGlyProLeuValLeuLysHis 1060
DB 3121 ATATATCTTTGACAAATGTAATTCATGTAAGTCCAGGTGGGCTCTGTACTGAAGCAT 3180
QY 1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGluAlaGly 1080
DB 3181 CTGACGACACTCTTAATCAACAGAAAGCTTGGATGTGGAAAGAACCGAGCTGA 3240
QY 1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100
DB 3241 AAAAGTTCCTCATCTCAGCCCTTTTATGATGTGCAAGAACCGAAGTAAATTTGGATT 3300
QY 1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysMetSerIleIle 1120
DB 3301 GATTAAGATCTTGACAACTGAATTTGACATTCATTAAGAAAGAAATGTCATCAATCA 3360
QY 1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
DB 3361 CCTCAGGAACCTGTTTGTCTTCACTGCAACATGAGAAAGAAACCTGATCCCTTAATG 3420
QY 1141 HisThrAspGluGluLeuThrPheAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160
DB 3421 CACACGATGAGGAAGTGTGAATGCTTACAAAGAGTCAACTTAAGAAACCATTTGA 3480
QY 1161 AspLeuProGlyLysMetAspThrGluLeuAlaGlnSerGlySerAsnMetSerValGly 1180
DB 3481 GATCTTCCGTAATAATGATGTAATTAAGCAATTCAGAAATCAATTTAGTGTGGA 3540
QY 1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
DB 3541 CAAGGCAACTGCTGTGCTTCCAGGCAATTCAGGAAATATCAATATGATTAAT 3600
QY 1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220
DB 3601 GATGAAGCAGCGCAATGATGATCCAGAACTGATGATTAATCAAAAAAATCCCG 3660
QY 1221 GluLysPheAlaHisGlyThrValLeuThrIleAlaHisArgLeuSerThrIleLeuAsp 1240
DB 3661 GAGAAATTTGGCCCATGACACGCTGACCATTTGACACAGATTTGAACCATTAATTTGAC 3720
QY 1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
DB 3721 AGGGAACAAGTAATGTTTATGATTCAGGAAGCATGAAGAAATATATGATGCGGTATGTT 3780
QY 1261 LeuLeuGlnAsnLysGlnSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280

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DB 3781 TTTGCTGCAAAATTAAGAGAGCTATTATTAAGATGGTGCAACACTGGGCAAGCAAA 3840
QY 1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysAsnTyrProHisIle 1300
DB 3841 GCCGCTGCCCTCAGCAAGAAACAGAAACAGATATCTTCAAGAAATTAATCAATATT 3900
QY 1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
DB 3901 GGTCACTGACCAATGTTTAAACAACTTCATATGACAGCCCTGCACCTTAATTAAT 3960
QY 1321 PheGluThrAlaLeu 1325
DB 3961 TTCGAGACAGCACTG 3975
RESULT 3
ADH10611
ID ADH10611 standard; DNA; 5271 BP.
XX
AC ADH10611;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human cancer-related polynucleotide, SEQ ID 1.
XX
KW Cancer-related gene; prostate cancer; cytosolic; human; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003104404-A2.
XX
PD 18-DEC-2003.
XX
PF 05-JUN-2003; 2003WO-US017772.
XX
PR 06-JUN-2002; 2002US-0386651P.
XX
PA (AVAL-) AVALON PHARM INC.
XX
PI Ebner R.
XX
DR WPI; 2004-062332/06.
XX
PT Identifying agents that modulate the activity of cancer-related gene,
PT useful for treating or diagnosing prostate cancer comprising contacting a
PT compound with a cell containing a gene under conditions promoting a
PT expression of the gene.
XX
PS Claim 1; SEQ ID NO 1; 79pp; English.
XX
CC The invention relates to identifying an agent that modulates the activity
CC of a cancer-related gene. The method involves contacting a compound with
CC a cell containing a gene that corresponds to a polynucleotide having a
CC sequence selected from (SEQ ID NO. 1-18) under conditions promoting the
CC expression of the gene. The method is useful for identifying an agent
CC that modulates the activity of a cancer-related gene. The polypeptides
CC and antibodies of the invention are useful for treating and diagnosing
CC cancer, preferably prostate cancer. It is also useful for screening
CC assays for agents that are effective in reducing the activity of cancer-
CC related genes. The present sequence represents a specific example of a
CC cancer-related polynucleotide sequence.
XX
SQ Sequence 5271 BP; 1480 A; 1087 C; 1212 G; 1492 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 0 Length: 5271
Score: 6785.00 Matches: 1324
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 99.9% Mismatches: 0
Query Match: 99.9% Indels: 0
DB: 12 Gaps: 0
US-09-976-858-42 (1-1325) x ADH10611 (1-5271)

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QY MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20  
 Db ATGCGCCCGGTTCACAGAGGTGAAGCCCAACCGCTGCAGAGCGCAACATCTGCCTCA 175  
 QY ArgValIlePhePheTrpLeuAsnProLeuPheLysIleGlyValLysArgArgLeuGln 40  
 Db CGCGGTCTTCTTGGGGGTCAATCCCTGTTTAAATGGCCATTAACGAGATTAAGG 235  
 QY GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60  
 Db GAAGATGATGTATGTATTCAGTGTCCAGAGAACCCCTCAACGACCTTGGAGAGAGTTGG 295  
 QY GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80  
 Db CAAAGGTTCGGGATTAAGAGATTTTAAAGCTGAGAAATGACGACAGAAAGCTTCTTTA 355  
 QY ThrArgAlaIleIleLysCysTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100  
 Db ACAAGAGCATCATTAAGTGTACCTGGAATCTTATTAAGTTTGGAAATTTTACGTTA 415  
 QY IleGlnLysSerAlaLysValIleGlnProIlePheLeuGlyLysIleLeuAsnTyrPhe 120  
 Db ATTGAGAAAGTGCACAAAGTATCCAGCCCATATTTTGGGAAATATTAATTAATTTT 475  
 QY GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140  
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 QY LeuThrPheCysThrLeuIleLeuAlaIleLeuHisIleLeuTyrPheTyrHisValGln 160  
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 QY CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180  
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 QY AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgLysMetAsn 320  
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QY ValArgLeuThrValThrLeuPhePheProSerAlaIleGlnArgValSerGlnAlaIle 380  
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QY PheGlnThrAlaLeu 1325
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Db TTCGAGACAGCACTG 4090
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RESULT 4  
 ADH10612  
 ID ADH10612 standard; DNA; 5284 BP.  
 XX  
 AC ADH10612;  
 XX  
 DT 11-MAR-2004 (first entry)  
 XX  
 DE Human cancer-related polynucleotide, SEQ ID 2.  
 KW Cancer-related gene; prostate cancer; cytostatic; human; gene; ds.  
 OS Homo sapiens.  
 XX  
 PN WO2003104404-A2.  
 XX  
 PD 18-DEC-2003.  
 XX  
 PF 05-JUN-2003; 2003WO-US017772.  
 XX  
 PR 06-JUN-2002; 2002US-0386651P.  
 XX  
 PA (AVAL-) AVALON PHARM INC.

XX Ebner R;  
XX MPI: 2004-062332/06.  
XX  
XX  
XX Identifying agents that modulate the activity of cancer-related gene,  
XX useful for creating or diagnosing prostate cancer comprising contacting a  
XX compound with a cell containing a gene under conditions promoting  
XX expression of the gene.

PS Claim 1; SEQ ID NO 2; 79pp; English.

XX The invention relates to identifying an agent that modulates the activity  
XX of a cancer-related gene. The method involves contacting a compound with  
XX a cell containing a gene that corresponds to a polynucleotide having a  
XX sequence selected from (SEQ ID NO. 1-18) under conditions promoting the  
XX expression of the gene. The method is useful for identifying an agent  
XX that modulates the activity of a cancer-related gene. The polypeptides  
XX and antibodies of the invention are useful for treating and diagnosing  
XX cancer, preferably prostate cancer. It is also useful for screening  
XX assays for agents that are effective in reducing the activity of cancer-  
XX related genes. The present sequence represents a specific example of a  
XX cancer-related polynucleotide sequence.

XX Sequence 5284 BP; 1480 A; 1138 C; 1210 G; 1456 T; 0 U; 0 Other;

# Alignment Scores:

Pred. No.: 0 Length: 5284  
Score: 6785.00 Matches: 1324  
Percent Similarity: 100.0% Conservative: 1  
Best Local Similarity: 99.9% Mismatches: 0  
Query Match: 99.9% Indels: 0  
DB: 12 Gaps: 0

US-09-976-858-42 (1-1325) x ADH10612 (1-5284)

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QY 21 ArgValPhePheTyrTrpLeuAsnProLeuPheLysIleGlyAlaLysArgArgLeuGlu 40  
DB 176 CGCGGTCTTCTGGTGGCTCAATCCCTGTTAAATGGCCATTAACGAGATTAGAG 235  
QY 41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluLeu 60  
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QY 61 GlnGlyPheTyrPhePheLysGluValLeuArgAlaGluAspAlaGlnLysProSerLeu 80  
DB 296 CAAAGGTTCTGGAGTAAAGAGTTTAAAGCTGAGATGACGSCACAGAGCCCTTCTTAA 355  
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DB 356 ACAAGAGCAATCATTAAGTGTACTGAAATCTTATTAGTTTGGAAATTTTACGTTA 415  
QY 101 IleGluGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleLeuAsnTyrPhe 120  
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QY 121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140  
DB 476 GAAATTTATGATCCATGATTTCTGGCTTTGAACACAGCCTAGCCCTTAGCCGAGTG 535  
QY 141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisIleLeuTyrPheTyrHisValGln 160  
DB 536 CTGACTTTTGGACGCTCATTTTGGCTAATCTGACATCACTTATATTTTATCAGCTTCA 595  
QY 161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180  
DB 596 TGTGTGGAGTGAAGGTTACGAGTACCATGTGCCATATGATTTTATCGAAGGCACTTGT 655  
QY 181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsn 200

DB 656 CTTAGTAACTATGCGCATGGGAGAGCAACACAGGCCGATATGCAATCTGCTGCCAAT 715  
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DB 716 GATGTGAACAAATTGATGACAGGTGACAGTGTCTTACCTTCCGTGGGACAGACACTG 775  
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Qy 861 IleProThrIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuValArg 880  
Db 2696 ATTCCTTGATCGCAATACCTTGGTTCCTCCCTTGAATCATTTTCTTTCTTGGCGCA 2755  
Qy 881 TyrPheLeuGluThrSerArgAspValValArgLeuGluSerThrIleArgSerProVal 900  
Db 2756 TATTTTGGAAACGTCAGAGATGTGAAGCGCTGGAATCTACAACTCGGAGTCCAGTG 2815  
Qy 901 PheSerHisLeuSerSerLeuGlnGlyLeuIleThrIleArgAlaIleTyrValAlaGlu 920  
Db 2816 TTTTCCACATTGATCTCTCTCCAGGGGCTCTGACCATCCGGGCAATACAAAGACAA 2875

Qy 921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaIleThrPheLeu 940  
Db 2876 GAGAGGTGTCAAGAACTGTTGATGATGACACCAAGATTTACATTCAGAGGCTTGGTTCTTG 2935  
Qy 941 PheLeuThrThrSerArgIleThrPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960  
Db 2936 TTTTGGACAAAGTCCCGCTGGTTCGCCCTCGCTGATGATGCTGTGGCAATGTTGTGC 2995  
Qy 961 IleIleValAlaPheGlySerLeuIleLeuAlaValSerThrLeuAspAlaGlyValValGly 980  
Db 2996 ATCATCTGCTGCTTTGGTCCCTGATCTTGGCAAAACCTCTGATGCCGGCAGAGTTGCT 3055  
Qy 981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnIleProCysValArgGlnSer 1000  
Db 3056 TTGGCACTGCTCTTATGCCCTCAGCTGATGAGGAGATGTTTCAAGTGTGTGTGCAAAAGT 3115  
Qy 1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020  
Db 3116 GCTGAAGTTGAATATGATGATCTCAGTAGAAAGGTCATTGAATACACAGACCTTGAA 3175  
Qy 1021 LysGluAlaProThrGluTyrGluValSerProProAlaIleProHisGluGlyVal 1040  
Db 3176 AAGAGAGACCTTGGGAATATCAGAAAGCCACACACAGCTGGCCCATGAAGAGTG 3235  
Qy 1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuValHis 1060  
Db 3236 ATTAATCTTGACAAATGTGAATTCATGTATACAGTCCAGGTGGGCTCTGGTACTGAAGCAT 3295  
Qy 1061 LeuThrAlaLeuIleLeuSerGlnGluValGlyIleValGlyArgThrGlyAlaGly 1080  
Db 3296 CTGACAGACCTCATTAATATCAACAAGAAAGTTGGCATTTGGGAAAGAACCGAGCTGGA 3355  
Qy 1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyValIleProIle 1100  
Db 3356 AAAAGTTCCCTCATCTCAGCCCTTTTGTAGATTGTTCAGAACCCGAAGCTTAATTTGGATT 3415  
Qy 1101 AspIleValLeuThrThrGluIleGlyLeuHisAspLeuArgIleValMetSerIleIle 1120  
Db 3416 GATTAAGATCTTGACAACTGAAGAAATTTGACTTCAGATTTAAGGAAGAAATGCAATCATATA 3475  
Qy 1121 ProGlnGluProValLeuPheThrGlyThrMetArgValAsnLeuAspProPheAsnGlu 1140  
Db 3476 CCTCAGGAACCTGTTTGTGTCTGTAAGCAAAAGAGAAAGAACCTGATCCCTTAATAGAG 3535  
Qy 1141 HisThrAspGluGluLeuThrPheAlaLeuGlnGluValGlnLeuValSerGluThrIleGlu 1160  
Db 3536 CACACGGATGAGAACTGTGAATCTCTTACAGAGGTACAACTTAAGAAACCATTTGA 3595  
Qy 1161 AspLeuProGlyValMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180  
Db 3596 GATCTTCCGTGAATATGGAATCTGATTAAGACAGATCAGATCCAAATTTTGTGTGGA 3655  
Qy 1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgValAsnGlnIleLeuIleIle 1200  
Db 3656 CAAGAACAACGTGTGTGCTTGGCCAGGGCAATTTCCAGGAAAAACAGATATTTGATTTAT 3715  
Qy 1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnValSerIleArg 1220  
Db 3716 GATGAAGCAGCGCAATGTGATCCAGAACCTGATGACTTAATCAAAAAAATCCCG 3775  
Qy 1221 GluValPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240  
Db 3776 GAGAAATTTGCCACGTGACACCGTGTACCATTTGACACAGATGGAACCACTTATTGAC 3835  
Qy 1241 SerAspIleValMetValLeuAspSerGlyValGluValGluTyrAspGluProTyrVal 1260  
Db 3836 ACCGACAGATATATGTTTATATTCAGGAAACCTGAAGAAATATATGATGACCGTATGTT 3895  
Qy 1261 LeuLeuGlnAsnValGluSerLeuPheTyrIleValGlnGlnLeuGlnValValAlaGlu 1280  
Db 3896 TTGCTGCATAATTAAGAGAGCTTATTTTACAGATGTGTCAACAACTGGGCAAGCGACAGA 3955

QY 1281 AaalaaleuthrGluthrAlaIySglnValIyRphelyARgAsnTyRProHisile 1300  
 DB 3956 GCCGCTGCCCTCCTACACGAAACAGCAACGGTACTTCAAAAGAAATTAATTCACATATT 4015  
 QY 1301 GlnHistrAAspHisMetValThrAnthrSerAnGlyGlnProSerThrLeuThrile 1320  
 DB 4016 GGTCACTACGACCAATGTTTCAAAACATTCATATGACAGCCCTGACCTTAATCTATT 4075  
 QY 1321 PheGluThrAlaLeu 1325  
 DB 4076 TTCGAGACGACACTG 4090  
 RESULT 5  
 ADH10624  
 ID ADH10624 standard; DNA; 5833 BP.  
 AC ADH10624;  
 XX 11-MAR-2004 (first entry)  
 DT 11-MAR-2004  
 XX Human cancer-related polynucleotide, SEQ ID 14.  
 DE Human cancer-related polynucleotide, SEQ ID 14.  
 XX Cancer-related gene; prostate cancer; cytostatic; human; gene; ds.  
 KW Homo sapiens.  
 OS Homo sapiens.  
 XX WO2003104404-A2.  
 EN 18-DEC-2003.  
 PD 05-JUN-2003; 2003WO-US017772.  
 PF 06-JUN-2002; 2002US-0386651P.  
 PR (AVAL-) AVALON PHARM INC.  
 XX Ebner R;  
 PI WPI; 2004-062332/06.  
 XX Identifying agents that modulate the activity of cancer-related gene,  
 PT useful for treating or diagnosing prostate cancer comprising contacting a  
 PT compound with a cell containing a gene under conditions promoting  
 PT expression of the gene.  
 XX Claim 1; SEQ ID NO 14; 79pp; English.  
 PS The invention relates to identifying an agent that modulates the activity  
 CC of a cancer-related gene. The method involves contacting a compound with  
 CC a cell containing a gene that corresponds to a polynucleotide having a  
 CC sequence selected from (SEQ ID NO. 1-18) under conditions promoting the  
 CC expression of the gene. The method is useful for identifying an agent  
 CC that modulates the activity of a cancer-related gene. The polypeptides  
 CC and antibodies of the invention are useful for treating and diagnosing  
 CC cancer, preferably prostate cancer. It is also useful for screening  
 CC assays for agents that are effective in reducing the activity of cancer-  
 CC related genes. The present sequence represents a specific example of a  
 CC cancer-related polynucleotide sequence.  
 XX  
 SQ Sequence 5833 BP; 1660 A; 1175 C; 1306 G; 1692 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 0 Length: 5833  
 Score: 6785.00 Matches: 1324  
 Percent Similarity: 100.0% Conservative: 1  
 Best Local Similarity: 99.9% Mismatches: 0  
 Query Match: 12 Gaps: 0  
 US-09-976-858-42 (1-1325) x ADH10624 (1-5833)  
 QY 1 MetLeuProValIyGlnGluValIySPProAnProLeuGlnAspAlaAsnLeuCySer 20  
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DB 116 ATGCTCCCGGTGACCAAGAGGTGAAGCCCAACCCGCTGACAGACCGCAACATCTGCTCA 175  
 QY 21 ArgValAPhePheTPTPTLeuAsnProLeuPheValIleGlnIleValArgArgLeuGlu 40  
 DB 176 CGCGGTCTCTTGCTGCTCAATCTCTGTTTAAATTTGGCAATTAACGGAGATTAGG 235  
 QY 41 GluAspAPMeTYSerValLeuProGluAspArgSerGlnIleLeuGlyValGluLeu 60  
 DB 236 GAGATGATATGATATTCAGTGTGCTGCCAAGAACCCCTCAGACACCTTGAGAGAGATTG 295  
 QY 61 GlnGlyPheTTPAspIySglnValIleuArgAlaGluAsnAspAlaGlnIySPProSerLeu 80  
 DB 296 CAAGGCTTCGAGATTAAGAAAGTTTAAAGCTGAGATGAGACAGACAGGCTTCTTA 355  
 QY 81 ThrArgAlaIleIleIySglnValIleuArgAlaGluAsnAspAlaGlnIySPProSerLeu 100  
 DB 356 ACAAGACAACTATTAAGTGTTCAGAAATCTTATTTAGTTTGGAAATTTTACGTTA 415  
 QY 101 IleGluGluSerAlaIySglnValIleuArgAlaGluAsnAspAlaGlnIySPProSerLeu 120  
 DB 416 ATTGAGAAAGTGCCTCAAGATTAATCCAGCCATATTTTGGAAAAATTTATTAATTTT 475  
 QY 121 GluAsnTYrAspProMetAspSerValAlaLeuAsnThrAlaTYrAlaTYrAlaThrVal 140  
 DB 476 GAAATTTATGATCCATGATTCGTGCTTGAACACAGCGTACGCCATGCAAGGTTG 535  
 QY 141 LeuThrPheCYThrLeuIleLeuAlaIleLeuHISLeuTYrPheTYrHISValGln 160  
 DB 536 CTGACTTTTTCACCGCTCATTTTGGCTATACGCACTCATATTTTATCATCCTTACG 595  
 QY 161 CysAlaGlyMetArgLeuArgValAlaMetCysHISMetIleTYrArgIySglnAlaLeuArg 180  
 DB 596 TGTGCTGAGATGAGGTTCAGATGACATGTCATGATGATTTATTCGAGAGCACTTGT 655  
 QY 181 LeuSerAsnMetAlaMetGlyIySglnValIleuArgAlaGluAsnAspAlaGlnIySPProSerLeu 200  
 DB 656 CTATGATTAACATGCGCATGCGGAGAACCAACAGCCAGATGATGATCTGCTGCAAT 715  
 QY 201 AspValAsnIySPProMetAspSerValAlaLeuAsnThrAlaTYrAlaTYrAlaThrVal 220  
 DB 716 GATGTGAACAAGTTTGATGACGTGACAGTGTCTTACCTCTGCTGCGACAGACACATG 775  
 QY 221 GlnAlaIleAlaValIleuLeuLeuThrPheGlnIleGlyIleSerCYLeuAlaGly 240  
 DB 776 CAGCGATGACGATGCTGCTCTCTGATGATGATGATGATGATGATGATGATGATGATG 835  
 QY 241 MetAlaValIleuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 260  
 DB 836 ATGCAAGTTTATATCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 895  
 QY 261 LeuArgSerIySPProMetAspSerValAlaLeuAsnThrAlaTYrAlaTYrAlaThrVal 280  
 DB 896 CTGAGAGATTAAGTGAACATCTTCAAGATGATGATGATGATGATGATGATGATGATGATG 955  
 QY 281 ThrGlyIleAlaGlyIleIleIySglnValIleuArgAlaGluAsnAspAlaGlnIySPProSerLeu 300  
 DB 956 ACTGATTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1015  
 QY 301 AsnLeuArgIySglnValIleuArgAlaGluAsnAspAlaGlnIySPProSerLeu 320  
 DB 1016 AATTTGAGAAAGAGAGATTTCCAGATTTCCAGATTTCCAGATTTCCAGATTTCCAGATTT 1075  
 QY 321 LeuAlaSerPhePheSerAlaSerIySglnValIleuArgAlaGluAsnAspAlaGlnIySPProSerLeu 340  
 DB 1076 TTGGCTTGTGTTTTCAGAGCAAGCAAAATCATCGTTTGGACCTTCAACCACTTACGCG 1135  
 QY 341 LeuLeuGlySerValIleuArgAlaGluAsnAspAlaGlnIySPProSerLeu 360  
 DB 1136 CTCTCTGCGAGGTGATACAGCCAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1195  
 QY 361 ValArgLeuThrValIleuArgAlaGluAsnAspAlaGlnIySPProSerLeu 380  
 DB 1196 GTGGCGCTGAGAGGTTACCTCTTCTTCCCTCAGCATTTGAGAGGCTGTCAGAGCAATC 1255

QY 381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400  
DB 1256 GTCACATCCGAAGATCCAGACCTTTTGTACTTGATGAGATATCAACAGGCAACGCT 1315  
QY 401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420  
DB 1316 CAGCTGCCGTCAAGATGTGTAAAAAGATGTGTCAATGTGCAGATTTTATCTCTTTTGGGAT 1375  
QY 421 LysAlaSerGluThrProThrIleuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440  
DB 1376 AAGGATCAAGAACCCCACTTACAGGCTTTCTTTACTGTCAAGCTTGCGAATTG 1435  
QY 441 LeuAlaValAlaGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValIleuGly 460  
DB 1436 TTAGCTGTGTGTCGCCCGCTGGAGAGAGAAAGTATCATCTGTAAAGTCCGTCGCGG 1495  
QY 461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480  
DB 1496 GAATTGGCCCCAAGTCAACGGCTGTGTCAAGCTGTCAAGAAATTCCTATGTGTCTCAG 1555  
QY 481 GlnProTrpValPheSerGlyThrIleuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500  
DB 1556 CAGCCCTGGGTGTCTCGGAACTCTGAGAGATTAATTTTATTTGGGAAAGAAATAGAA 1615  
QY 501 LysGluArgTyrGlyLysValIleLysAlaCysAlaLeuLysAspLeuGlnLeuLeu 520  
DB 1616 AAGGAACGATGAAAAAGTCAATAAGCTTGTGTCTGAAAAAGATTTACAGCTGTG 1675  
QY 521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540  
DB 1676 GAGGATGGGATCTGACTGTGTAGAGATCGGGAAACCACTGTGTAGAGGGCGAA 1735  
QY 541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560  
DB 1736 GACGGGTAACTTTCAGAGAGAGATGTATCAAGATCTGACATCTATCTCTGAGCAT 1795  
QY 561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGlyLysCysGln 580  
DB 1796 CCTCTCAGTGCAGTGAATCGGAGATTAGACAGACCTTGTGAACTGTGTATTTGTGCA 1855  
QY 581 IleLeuHisGlyLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600  
DB 1856 ATTTTGCATGAGAAAGATCACAATTTTATGACTCATCACTGACATCTCAAGCTGTGA 1915  
QY 601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620  
DB 1916 AGTCAGATTCTGATATTGAAGATGTGTAAATGTGTCAAGAGGGACCTTACCTGAGTTC 1975  
QY 621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGlnLeuSerGlnGln 640  
DB 1976 CTAAATATCGTATATGATTTTGGCTCCCTTTTAAAGAGATATATGAGAAAGTGAACA 2035  
QY 641 ProProValProGlyThrProThrIleuArgAsnArgThrPheSerGlnSerSerValTrp 660  
DB 2036 CCTCCAGTTCACGAGAACTCCCACTAAAGAAATCGTATCTTCAAGAGCTTCGCTGG 2095  
QY 661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGlnSerGlnAspThrGln 680  
DB 2096 TCTCAACATCTTCTAGACCTCTCTTGAAGATGTGTCTGTGAGAGCCAAAGTATCAGAG 2155  
QY 681 AsnValProValThrLeuSerGlnGluAsnArgSerGlnGlyLysValGlyPheGlnAla 700  
DB 2156 AATGTCACGATTACACTATCAAGAGAAACCGTTCGAAAGAAAGTTGGTTTTTCAGGCC 2215  
QY 701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValAlaPheIlePheLeuIleLeuLeu 720  
DB 2216 TATTAAGAAATTAATCTCAGAGCTGTGTCTCACTGATTTCTCATTTTCTTATTTCTCCA 2275  
QY 721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740  
DB 2276 AACACTGCAGCTCAGGTGTCTATGTGTCTTCAAGATTTGGCTTTCATATCAGGGCAAC 2335

QY 741 LysGlnSerMetLeuAsnValThrValIsnGlyGlyLysAsnValThrGluLysLeuAsp 760  
DB 2336 AAACAAAGTATGCTAAATGTCATCTGAATGAGAGAGAAATGTAAACGAGAAAGCTAGAT 2395  
QY 761 LeuAsnTrpTyrLeuGlyIleGlySerGlyLeuThrValAlaThrValLeuPheGlyIle 780  
DB 2396 CTAACTGTACTTGAAGATTAATTCAGGTTTAACTGTAGCTTACCTTTTGGCATTA 2455  
QY 781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800  
DB 2456 GCAAGATCTATATGATTTTCAAGTCCCTGTATACCTTTCACAAACCTTGCACAAACAA 2515  
QY 801 MetPheGlnSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820  
DB 2516 ATGTTTGATCAATCTGAAGCTCCGGTATTAATCTTGTGTAGAAATCCATATAGAAAG 2575  
QY 821 IleLeuAsnArgPheSerLysAspIleGlyHisIleLeuAspAspLeuLeuProLeuThrPhe 840  
DB 2576 ATTTTAAATCGTTTCTCAAGACATTTGACACTTGGATGATTTGCTGCGCTGCGCTTT 2635  
QY 841 LeuAspPheIleGlnThrLeuLeuGlnValAlaGlyValAlaSerValAlaValAlaVal 860  
DB 2636 TTAGATTTCAATCAACAAATTTGCTTACAGTGTGTGTGTGTCTGTGTGCTGTGCGCG 2695  
QY 861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880  
DB 2696 ATTCCTTGATTCGAATACCTTGTGTCCCTTGTGAATCATATTTTCATTTTCTTGGCGA 2755  
QY 881 TyrPheLeuGlnThrSerArgAspValLysArgLeuGlnSerThrThrArgSerProVal 900  
DB 2756 TATTTTGGAAACGTCAAGATGTAAAGCCCTGGAATCTTCAACTCGAAGTCAAGT 2815  
QY 901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920  
DB 2816 TTTTCCCACTGTATCTTCTCTCCAGGGGCTCTGAGCATCCGGGCAATACAAACAGAA 2875  
QY 921 GluArgCysGlnGlnLeuPheAspAlaHisGlnAspLeuHisLeuSerGluAlaTrpPheLeu 940  
DB 2876 GAGAGGTTCAGGAATGTTGTATGATCACACCGAGTTTACATTCAGAGCTTGTGTTCTTG 2935  
QY 941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960  
DB 2936 TTTTGGACAGCTCCCGGTGGTGTGCGCTGTGTGAGATGCCATCTGTGCCATGTGTTGTC 2995  
QY 961 IleIleValAlaPheGlySerLeuIleLeuAlaTyrThrLeuAspAlaGlyGlnValGly 980  
DB 2996 ATCATCGTTCCTTGGGTCCCTGATTTCTGGAAAACTCTGGATCCGGGAGGTGTGT 3055  
QY 981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000  
DB 3056 TTGGCACTGTCTTATGCTCTCAAGCTCATGTGGGATGTTTCAGTGTGTGTGTGCAAAAGT 3115  
QY 1001 AlaGluValGluAsnMetMetIleSerValGluArgValIleGlnTyrThrAspLeuGln 1020  
DB 3116 GCTGAAGTTGAAGAAATGATGTCTCAGTGAAGAAAGGTCAATTGAATACAGACTTGA 3175  
QY 1021 LysGluAlaProTrpGluTyrGlnLysArgProProAlaTrpProHisGlnGlyVal 1040  
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QY 1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060  
DB 3236 ATTAATCTTTGACAAATGTGAACCTTCAATGTCAAGGTGGGCTCTGTGTACTGAAGCAT 3295  
QY 1061 LeuThrAlaLeuIleLysSerGlnGlyLysValGlyIleValGlyArgThrGlyAlaGly 1080  
DB 3296 CTGACAGCACTATTAATCAAGAAAGGTTGGATTTGTGGAAAGAACCGAGCTGGA 3355  
QY 1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100  
DB 3356 AAAAGTCCCTCATCTCAGCCCTTTTATGATTTGTCAAGAACCGGAAGGTAAATTTGGAT 3415  
QY 1101 AspLysIleLeuThrThrGlnIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120



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DB 3416 GATTAGATCTTACACGATTAATGACCTTACGATTTTAAGAGAAATGTCATCA 3475
QY 1121 PROGLINGUProValleuPheThrglyThrMetAglValleuPheProPheanGlu 1140
DB 3476 CCGAGGAACTGTTTGTTCCTGACCTGACCAAGAGAAAACCTGATCCCTTTATGAG 3535
QY 1141 HISTRAPGluGluLeuThrPheValleuGluGluValleuGluLeuGluThrlleGlu 1160
DB 3536 CACAGGATGAGAACTGTGAACTGCTTACAGAGGTAACAATTAAAGAAACCAATTGA 3595
QY 1161 AspLeuProGluValMetAspThrgluLeuValleuGluSerGluSerAspPheSerValGly 1180
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QY 1181 GluValGluLeuValCysLeuValleuValleuValleuValleuValleuValleu 1200
DB 3656 CAAGAGCAACTGTGTGCTTCCAGGCGCAATTCAGGAAAATCAGATATTGATTAT 3715
QY 1201 ABPGluValThrAlaValleuAspProArgThrgluLeuGluLeuValleuValleu 1220
DB 3716 GATGAAGCGAGCGCAATGTGATTCAGAGACTGATGATTAATCAAAAAAATCCGG 3775
QY 1221 GluValPheAlaHisCysThrValleuThrlleAlaHisArgLeuAsnThrlleLeuAsp 1240
DB 3776 GAGAAATTTGCCCATCGACCGCTGTAACCATTTGACACAGATTTGAACCATTTGAC 3835
QY 1241 SerAspValleuMetValleuAspSerGluValleuValleuValleuValleuValleu 1260
DB 3836 AGCGCAAGATTAATGTTTATGATTCAGGAAAGATTAAGATGAGCCGATGTT 3895
QY 1281 LeuLeuGluAsnValleuGluSerLeuPheThrlleValleuValleuValleuValleu 1280
DB 3896 TTGCGCAAAATTAAGAGAGCTTATTTTCAAGATGTGCAACAATGGGCAAGGCAAGA 3955
QY 1281 AlaAlaAlaLeuThrgluThrlleValleuValleuValleuValleuValleuValleu 1300
DB 3956 GCCGCTGCCCTCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 4015
QY 1301 GlyHisThrAspPheMetValleuThrlleValleuValleuValleuValleuValleu 1320
DB 4016 GGTTCACATGACCAATGTTTCAAAACATTCATGACAGCCCTGACCTTAAT 4075
QY 1321 PheGluThrlleValleu 1325
DB 4076 TTCGAGACGACCTG 4090

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RESULT 6  
ADH10626  
ID ADH10626 standard; DNA; 5862 BP.

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XX ADH10626;
XX AC ADH10626;
XX DT 11-MAR-2004 (first entry)
XX DE Human cancer-related polynucleotide, SEQ ID 16.
XX KW Cancer-related gene; prostate cancer; cytosolic; human; gene; ds.
XX OS Homo sapiens.
XX PN WO2003104404-A2.
XX PD 18-DEC-2003.
XX PF 05-JUN-2003; 2003WO-US017772.
XX PR 06-JUN-2002; 2002US-0386651P.
XX PA (AVAL-) AVALON PHARM INC.
XX PI Ebner R;
XX

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DR WPI, 2004-06232/06.
XX Identifying agents that modulate the activity of cancer-related gene,
PT useful for treating or diagnosing prostate cancer comprising contacting a
PT compound with a cell containing a gene under conditions promoting
XX expression of the gene.
PS Claim 1, SEQ ID NO 16; 79pp; English.
XX
CC The invention relates to identifying an agent that modulates the activity
CC of a cancer-related gene. The method involves contacting a compound with
CC a cell containing a gene that corresponds to a polynucleotide having a
CC sequence selected from (SEQ ID NO. 1-18) under conditions promoting the
CC expression of the gene. The method is useful for identifying an agent
CC that modulates the activity of a cancer-related gene. The polypeptides
CC and antibodies of the invention are useful for treating and diagnosing
CC cancer, preferably prostate cancer. It is also useful for screening
CC assays for agents that are effective in reducing the activity of cancer-
CC related genes. The present sequence represents a specific example of a
CC cancer-related polynucleotide sequence.
XX
SQ Sequence 5862 BP; 1645 A; 1208 C; 1328 G; 1681 T; 0 U; 0 Other;

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Alignment Scores:

Pred. No.:	Length:	Matches:	Mismatches:	Indels:	Gaps:
Score: 6785.00	5862	1324	1	0	0
Percent Similarity: 100.0%					
Best Local Similarity: 99.9%					
Query Match: 99.9%					
DB: 12					

US-09-976-858-42 (1-1325) x ADH10626 (1-5862)

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QY 21 ArgValPhePheThrllePheValleuPheValleuPheValleuPheValleuPhe 40
DB 176 GCGGTGTTCTGTGTGCTCAATCCCTGTTTAAATGGCCCAATTAAGAGATTAGAG 235
QY 41 GluAspAspMetValleuValleuProGluAspAspSerGluHisLeuGluValleu 60
DB 236 GAAATGATATGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 295
QY 61 GlnGlyPheThrllePheValleuValleuValleuValleuValleuValleuValleu 80
DB 296 CAAGGTTCTGGATTAAGAGAGTTTAAAGCTGAGATGACGACAGAGAGCTTCTTTA 355
QY 81 ThrArgAlaAlaLeuValleuValleuValleuValleuValleuValleuValleu 100
DB 356 ACAGAGCAATCATTAAGTGTGATGAGAACTTATTAAGTTTGGGAAATTTTAACTTA 415
QY 101 IleGluGluSerAlaValleuValleuProIlePheLeuGluValleuValleuValleu 120
DB 416 ATTGAGAAATGCGCAAGTAAATCAAGCCATATTTTGGGAAATTTTAAATTTT 475
QY 121 GluAsnValleuPheMetAspSerValleuValleuValleuValleuValleuValleu 140
DB 476 GAAATTAATGATCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 535
QY 141 LeuThrPheCysThrLeuValleuValleuValleuValleuValleuValleuValleu 160
DB 536 CTGACTTTTTCAGCGCTCAATTTTGGCTTACTGATGATGATGATGATGATGATGAT 595
QY 161 CysAlaGluMetArgLeuValleuValleuValleuValleuValleuValleuValleu 180
DB 596 TGTGCTGGAGAGGTTTACAGTACGATGATGATGATGATGATGATGATGATGATGAT 655
QY 181 LeuSerAsnMetAlaMetGluValleuThrlleValleuValleuValleuValleu 200
DB 656 CTTAGTAACATGCGCATGGGAGAGCAACACAGCGCGAGATGATCAATCTGCTGCAAT 715

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 Db 836 ATGGCAGTCTAATATCTCTCGGCCCTGCAAAAGCTGTTTGGGAAGTGTTCATATCA 895  
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Best Local Similarity: 99.9% Mismatches: 1  
 Query Match: 99.9% Indels: 0  
 DB: 14 Gaps: 0

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 41 GluAspAspMetTyrSerVal1LeuProGluAspArgSerGlnHisLeuGlyGluLeu 60  
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 61 GlnGlyPheTrpAspLysGluVal1LeuArg1AgLysAspAlaGlnLysProSerLeu 80  
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 101 IleGluGluSerAlaLysVal1IleGlnPro1LeuPheLeuGlyLys1LeuAsnTyrPhe 120  
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QY	741	LySGlnSerMetLeuAsnValThrValAsnGlyGlyIleAsnValThrGluLysLeuAsp	760
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QY	841	LeuAspPheIleGlnThrLeuLeuGlnValGlyValIleSerValAlaValAlaVal	860
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QY	861	IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuAspArg	880
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Oy		1301	GlyHisThrAspHisMetValIleAsnThrSerAsnGlyGlnProSerThrLeuThrIle	1320		
Dd		3908	GGTCACACTGACCAATAGTGTACAAACACTTCCAMATGACAGCCCTCGACCTTAACATATT	3967		
Oy		1321	PheGluThrAlaLeu 1325			
Dd		3968	TTGAGACAGCACTG 3982			
<b>RESULT 8</b>						
ID	AAZ30078	AAZ30078 standard; cDNA; 4231 BP.				
XX	AAZ30078;					
AC						
DT	26-JAN-2000	(first entry)				
XX						
DE	cDNA encoding a human MPR-related ABC transporter designated MOAT-B.					
KX	Human, MPR-related ABC transporter; MOAT protein, MOAT-B;					
KW	MOAT mediated transport; anticancer drug sensitivity;					
KM	transporter mediated cellular efflux; anticancer; ss.					
XX						
OS	Homo sapiens.					
XX						
PH	Key	Location/Qualifiers				
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XX      27-MAR-1998; 98US-0079759P.
XX      03-AUG-1998; 98US-0095153P.
XX      (FOXO-) FOX CHASE CANCER CENT.
XX      Krub G, Lee K, Belinsky M, Bain L;
XX      WPI, 1999-610812/52.
XX      P-PSDB; AAY43541.
PT      New transporter gene useful for screening for anti-cancer drugs.
PS      Claim 1; Page 130-131; 153pp; English.
XX      The present sequence encodes a human MPR-related ABC transporter (MOAT)
XX      protein, designated MOAT-B. The protein comprises a multi-domain
XX      structure including a tandem repeat of nucleotide binding folds appended
XX      C-terminal to a hydrophobic domain, having Walker A and B ATP binding
XX      sites and several potential membrane spanning domains. The MOAT nucleic
XX      acids are useful for screening a test compound for inhibition of MOAT
XX      mediated transport, indicated by restoration of anticancer drug
XX      sensitivity, which in turn causes a reduction of transporter mediated
XX      cellular efflux of anticancer agents. MOAT DNA or RNA may be used as
XX      probes to detect the presence or expression of genes encoding MOAT
XX      proteins. Anti-MOAT antibodies are useful for detecting and quantitating
XX      MOAT proteins
SQ      Sequence 4231 BP; 1170 A; 895 C; 1015 G; 1151 T; 0 U; 0 Other:

Alignment Scores:
Pred. No.: 0 Length: 4231
Score: 6779.00 Matches: 1323
Percent Similarity: 99.9% Conservative: 1
Best Local Similarity: 99.8% Mismatches: 1
Query Match: 99.9% Indels: 0
DB: 2 Gaps: 0

US-09-976-858-42 (1-1325) x AA230078 (1-4231)
QY      1 MetLeuProValTyrGlnGluValIlysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
DB      116 ATGCGCCCGGTGATCCAGAGGAGGAGCCCAACCCCTCGAGGACCGAACAATCGCTCA 175
QY      21 ArgValPhePheTrpTrpLeuAsnProLeuPheIleGlyHisIleArgArgLeuGln 40
DB      176 CCGGTGTTCTTCGGTGGCTCAATCCCTGTTTAAATGGCCATTAACGAGATTAGAG 235
QY      41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60
DB      236 GAGAGATATGATGATTCAGTGGCTGCCAGAAACCGCTCAAGCACCTTGAGAGGAGTGG 295
QY      61 GlnGlyPheTrpAspIleGluValIleuArgAlaGluAsnAspAlaGlnIysProSerLeu 80
DB      296 CAAGGGTTCTGGAGTAAAGAGTTTAAAGAGCTGAGAAATGACGACAGAAAGCCCTTTTAA 355
QY      81 ThrArgAlaIleIleIysCysTyrTrpIysSerTyrLeuValLeuGlyIlePheThrLeu 100
DB      356 ACAAGAGCATCATTAAGTGTACTGGAATCTTATTAGTTTGGGAATTTTACGTTA 415
QY      101 IleGluIleSerAlaIysValIleGlnProIlePheLeuGlyIleIleAsnTyrPhe 120

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DB      416 ATTGAGAAAGTGCAGAAAGTAATCCAGCCCATATTTTGGAAAAATATTAATTAATTTT 475
QY      121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaThrVal 140
DB      476 GAAATTTATGATCCCATGATGATTTCTGTGGCTTTGAACAAGGATGCGCTATGCCAGGG 535
QY      141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisIleLeuTyrPheTyrHisValGln 160
DB      536 CTGACTTTTTCACCCCTCATTTTGGCTTATGCTATGATCACTTAATTTTATCACTTCAG 595
QY      161 CysAlaGlyMetArgLeuAspValAlaMetCysHisMetCileTyrArgIleValAlaLeuArg 180
DB      596 TGTGCTGGAGATGAGTTACAGATGACCATGCGCATATGATTTATTCGAGAAGCACTTGCT 655
QY      181 LeuSerAsnMetAlaMetGlyIleThrThrThrGlyGlnIleValAsnLeuSerAsn 200
DB      656 CTTACTTAACATGCGCATGGGAGAGCAACAGCGCCAGATGATCAATCTGTGTCAT 715
QY      201 AspValAsnIlePheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
DB      716 GATGTGAACAAAGTTTGATCAGGTGACAGTGTCTTACACTTCTGTGGGACAGACACTG 775
QY      221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGlnIleGlyIleSerCysLeuAlaGly 240
DB      776 CAGGCGATGCGAGTGTGCTCCCTACTGTGATGAGATAGGAATTCGTGCTTCTGGG 835
QY      241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyIleLeuPheSerSer 260
DB      836 ATGGAGTTCTTATCATTTCTCTGCTTGGCAACCTGTTTGGGAAGTTGTCATCA 895
QY      261 LeuArgSerIleThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
DB      896 CTGAGAGCTGAATAACCGCAACTTTCACGATGCGAGATGACAGACCATGAATGAATTTTA 955
QY      281 ThrGlyIleArgIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 300
DB      956 ACTGTATTAAGATATTAATAATGTAACGCTGGGAAAAGTCAATTTTCAAACTTATTTACC 1015
QY      301 AsnLeuArgIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 320
DB      1016 AATTTGAGAAAGAGAGAGATTTCCAAAGATTCGAGAAATTCCTGCTCGAGGGAGTAAAT 1075
QY      321 LeuAlaSerPhePheSerAlaSerIleIleIleValPheValThrPheThrThrTyrVal 340
DB      1076 TTGGCTGTTGTTTTCAGTGAAGCAAAATCAATCGTTTGTGACCTTCAACCACTTACG 1135
QY      341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
DB      1136 CTCTCGGCGAGTGTATCAAGCCAGCCGCGTGTGAGGAGTGAAGCCGTATAGGGGCT 1195
QY      361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380
DB      1196 GTGGCGGTGACGGTATACCTCTTCTCCCTAGCACTTGAAGAGGTGTGAGAGCAATC 1255
QY      381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400
DB      1256 GTCAAGATCCGAAGATCAAGACCTTTTGTCACTTGTGATGATTCACAGCGCAACCGT 1315
QY      401 GlnLeuProSerArgGlyIleIleIleIleIleIleIleIleIleIleIleIleIleIle 420
DB      1316 CAGCTGCCGTCAAGATGTAAGTAAGTGTGAGAGATTTTACGCTTTTGGAGAT 1375
QY      421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440
DB      1376 AAGGATCAAGAGACCCCAACTTACAAGGCCCTTTCATCTGACAGCTGGGAAATTG 1435
QY      441 LeuAlaValIleGlyProValIleValIleGlyIleIleIleIleIleIleIleIleIle 460
DB      1436 TTAGCTGTGTGTGCGCCCGTGGAGACAGGAAATGATCATCTGTAAAGTCCGTGCTGGG 1495
QY      461 GluLeuAlaProSerHisGlyIleValSerValHisGlyArgGlyIleAlaTyrValSerGln 480
DB      1496 GAATTTGCCCAAGTCAAGGCTGTGTGAGCGTGTGATGAGAAAGATTCCTATGTGTCTAG 1555

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QY 481 GlnProTValPheSerGlyThrLeuArgSerAenIleLeuPheGlyValSerTyrGlu 500  
Db 1556 CAGCCCTGGGTTCTCGGAACTCTGAGAGTAATATTATTTGGGAAAGAAATATGAA 1615  
QY 501 LysGluArgTyrGluValIleValaCySaIaLeuValLeuAspLeuIleuLeu 520  
Db 1616 AAGGAACGATATGAAAAAGTCATAAAGCTTGCTGCTGAAAAGATTTACAGCTGTTG 1675  
QY 521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGluVal 540  
Db 1676 GAGGATGGGATCTGACTGTGATGAGAGATCCGGGAAACCACTGAGTGGAGGAGAAA 1735  
QY 541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560  
Db 1736 GCACGGGTAAACCTTGCAAGACAGTGTATCAAGATGTGACACTATCTCTCGACGAT 1795  
QY 561 ProLeuSerAlaValAspAlaGluValSerArgHlaLeuPheGlyLeuGlySerIleCysGln 580  
Db 1796 CCTCTCAGTGCAGTATGATGCGGAAGTTAGCAGACACTTCTGAACTGTGATTTGTCA 1855  
QY 581 IleuValIleGluValIleThrIleLeuValThrHlaGlnLeuGlnTyrLeuValAla 600  
Db 1856 ATTTTGCAATGAGAAATCACAATTTTAGTCACTCATGAGTTGCAAGTCAAGCTGCA 1915  
QY 601 SerGlnIleLeuIleLeuValAspGlyValSerMetValGlnValGlyThrTyrThrGluPhe 620  
Db 1916 AGTCAGATTCGATATGTGAAAGATGTGAAATGTGTGCAAGAGGGAAGCTTACAGTTC 1975  
QY 621 LeuValSerGlyIleAspPheGlySerLeuLeuValValAspAsnGluGluSerGluGln 640  
Db 1976 CTAAATCTGGATATGATTTTGCTCCCTTTAAAGAAAGATATAGAGAAAGTGAACA 2035  
QY 641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGluSerSerValTyr 660  
Db 2036 CCTCCAGTTCAGAACTCCCACTCAAGAAATCGATCTTCAGAGCTTCGGTGTGG 2095  
QY 661 SerGlnIleSerSerArgProSerLeuValAspGlyAlaLeuGlnSerGlnAspThrGlu 680  
Db 2096 TCTCAACAATCTTCAAGCCCTCTGAAAGATGTGTCTGTGAGAGCCCAACAATCAAG 2155  
QY 681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyValGlyValGlyPheGlnAla 700  
Db 2156 AATGTCAGTATCACTATCAAGAGAGAACCTTCTGAAGGAAAGACTTTTCAGGCC 2215  
QY 701 TyrIleAsnTyrPheArgAlaGlyAlaHlaIleTyrIleValPheIlePheLeuIleLeu 720  
Db 2216 TATAAGATTAATCTCAGAGCTGTGCTCACTGGAATGTCTTCATTTCTTATTCCTCA 2275  
QY 721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTyrTyrLeuSerTyrTyrAlaAsn 740  
Db 2276 AACACTGCAGCTCAGAGTGTCTATGTGCTTCAAGATGTGTGCTTCAATACAGGCGAAAC 2335  
QY 741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyValAsnValThrGluValLeuAsp 760  
Db 2336 AAACAAAGATCTAAATCTCACTGTAAATGAGAGAGAAATGTAAACCAAGACCTAGAT 2395  
QY 761 LeuAsnTyrTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780  
Db 2396 CTTAACGTGACTTGAATTTATTCAGGTTTAACTGATGCTAACGCTCTTTTGGCATA 2455  
QY 781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHlaAsnVal 800  
Db 2456 GCAAGATCTCTATGTATCTTACGCTCTGTATCTTCAACAACTTGTGACAAACAA 2515  
QY 801 MetPheGluSerIleLeuValAlaProValLeuPhePheAspArgAsnProIleGlyArg 820  
Db 2516 ATGTTTGACTCAATCTGAAGCTCCGGATATTTCTTTGATAGAAATCCATAGGAAGA 2575  
QY 821 IleLeuAsnArgPheSerValAspIleGlyHlaLeuAspAspLeuLeuProLeuThrPhe 840  
Db 2576 ATTTTAAATCGTTTCTCAAAAGACATGTGACACTGTGATGATTTGCTGCGCTGACGTTT 2635

QY 841 LeuAspPheIleGlnThrLeuGlnValValGlyValAlaValSerValAlaValAlaVal 860  
Db 2636 TTAGATTTCACTCAGACACTTGTCTACAACTGTGTGTGTCTCTGTGCTGTGACCGT 2695  
QY 861 IleProTyrIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880  
Db 2696 ATTCCTGGATCGCAATACCTCTGGTTCCTCTGGAAATCATTTTCATTTTCTTGGCGCA 2755  
QY 881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluGluSerThrThrArgSerProVal 900  
Db 2756 TATTTTGGAAACCTCAAGAGATGTGAAGCCCTGGAATCTACAACTCGAGTCCAGAG 2815  
QY 901 PheSerHlaLeuSerSerSerLeuGlnGlyLeuTyrThrIleArgAlaTyrValAlaGlu 920  
Db 2816 TTTTCCACTTGTCACTCTCTCTCCAGGGGCTCTGACATCCGGGCAATCAACACAGA 2875  
QY 921 GluArgGlyGlnGluLeuPheAspAlaHlaGlnAspLeuHlaSerGluAlaTyrPheLeu 940  
Db 2876 GAGAGGTGACAGAACTGTTGATGACACACAGATTTACATTCAGAGGCTGTGTTCTTG 2935  
QY 941 PheLeuThrThrSerArgTyrPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960  
Db 2936 TTTTGGACAGCTCCCGTGTGCGCGTCCGTGATGATGCCATGTGCGCATGTTTGTTC 2995  
QY 961 IleIleValAlaPheGlySerLeuIleLeuAlaValTyrThrLeuAspAlaGlyValValGly 980  
Db 2996 ATCATCGTTGCTTTGGTTCCTGATTTCTGGCAAAACTCTGATGCCGGAGAGTTGGT 3055  
QY 981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTyrCysValArgGlnSer 1000  
Db 3056 TTGGCACTGCTCTATGCCCTCAAGCTCAAGGGAATGTTCAAGTGTGTGACAAAGT 3115  
QY 1001 AlaGluValGluAsnMetMetIleSerValGluValIleGlnTyrThrAspLeuGlu 1020  
Db 3116 GCTGAAGTTGAGAAATATATATATCTCAGTATGAAGAGGTCATTAATACACAACTTGA 3175  
QY 1021 LysGluAlaProTyrGluTyrGluValAspArgProProAlaTyrProHlaGluGlyVal 1040  
Db 3176 AAAGAAACCTTGGGAATATCAAGAACGCCCAACCAAGCTGGCCCATGAAGAGAG 3235  
QY 1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuValHis 1060  
Db 3236 ATTAATCTTGACAAATGTGAATTCATGTATGATTCAGAGTGGGCTCTGTGATCTGAAGCAT 3295  
QY 1061 LeuThrAlaLeuIleLysSerGlnGluValGlyIleValGlyArgThrGlyAlaGly 1080  
Db 3296 CTGACAGACATCATTAATATCAACAGAAAGGTGGCATTTGGAGAAACCGGACCTGGA 3355  
QY 1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTyrIle 1100  
Db 3356 AAAAGTCCCTCATCTCAGCCCTTTTGTGATTTGTCAAGAACCGAAGGTAAATTTGAT 3415  
QY 1101 AspLysIleLeuThrThrGluIleGlyLeuHlaAspLeuArgLysLysMetSerIleIle 1120  
Db 3416 GATTAAGATCTTGACAACTGAATTTGACCTTCAGATTTAAAGAGAAATATGCAATCAT 3475  
QY 1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140  
Db 3476 CCTCAGGAACCTGTTTGTCTCTGGAACATAGAGAAAAACCTGATATCCCTTTTAAAGG 3535  
QY 1141 HisThrAspGluGluLeuTyrAsnAlaLeuGlnGluValGlnLeuValGluThrIleGlu 1160  
Db 3536 CACACGATAGAGAACTGTGAATCTCTTACAGAGGTACAACTTAAAGAAACCATTTGA 3595  
QY 1161 AspLeuProGlyLysMetAspThrGluLeuValGluSerGlySerAsnPheSerValGly 1180  
Db 3596 GATCTTCCGTGGAATATGATCTGATTTAGAGAGATCAGATTCATTTTATGTGTGGA 3655  
QY 1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuValGlyValAsnGlnIleLeuIleIle 1200  
Db 3656 CAAGACACATGTGTGTCTTGGCCAGGGCAATTCACAGAAAAATCAGATATATGATTTAT 3715  
QY 1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220



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DB      3716 GATGAGGACGCGCAAAATGTGATCCAGAACTGATGACTAATACAAAAAATCCGG 3775
QY      1221 GILVSPHEALAHISCyethrValleuthrIleahIaIeArgLeuBanthrIleleap 1240
DB      3776 GAGAAATTTGCCACCTGCACCGCTTAAACCATTTGACACAGATTGAAACCATTTATTGAC 3835
QY      1241 SerAPLYBILMeTValLeuBSPserGlyArgLeuVleGILTyRASPGLuProTyrVal 1260
DB      3836 ACCGACACAGATTAATGTTTAAATTCAGAAACCTGAAAGAAATATGATAGCCGATGTT 3895
QY      1261 LeuLeuGlnAsnLySGIuSerLeuPheTyrIlyMeTValGlnGlnLeuGlyIysAlaGlu 1280
DB      3896 TTGCTGCAAAATTAAGAGAGCCATTATTTCAAGATGTGTCAACAATGGGCAAGGACAGA 3955
QY      1281 AIAAIAIAleuthrGluThrAlaIySGInValTyrPheLyArgAsnTyrProHisIle 1300
DB      3956 GCCGCTGCCCTCACTGAAACAGCAAAACAGTATACCTTCAAAAAGAAATTAACACATATT 4015
QY      1301 GLYHISThrASPHisMeTValThraenThrSerAsnGlyGlnProSerThrLeuThrIle 1320
DB      4016 GGTCACTGACCACTGCTTACCAACACTTCCATGAGACAGCCCTCGACCTTAATT 4075
QY      1321 PheGluThrAlaLeu 1325
DB      4076 TTCAGACAGCACTG 4090

RESULT 9
AAH81778
ID      AAH81778 standard; DNA; 4231 BP.
AC      AAH81778;
XX      21-SBP-2001 (first entry)
DE      Human differential transcription-associated cDNA SEQ ID 287.
XX      Differential transcription; human; rat; tumour cell; cytostatic;
KM      Ras modulator; Class II tumour suppressor gene; gene therapy; ss.
XX      Homo sapiens.
OS      Homo sapiens.
XX      WO200157058-A2.
PN      09-AUG-2001.
XX      31-JAN-2001; 2001WO-BE001003.
XX      31-JAN-2000; 2000DE-01004102.
XX      (META-) METAGEN GES GENOMFORSCHUNG MBH.
PI      Rosenthal A, Hinzmann B, Schaefer R, Zuber J, Tchernitsa O;
PI      Grips M, Hellriegel M, Schmitz A, Sers C;
XX      WPI; 2001-483415/52.
XX      Nucleic acids differentially expressed between tumor and normal cells,
PT      useful for diagnosis or therapy of tumors and for screening active
PT      agents.
XX      Disclosure; Page 442-443; 579pp; German.
XX      This invention describes a nucleic acid (I) with differential expression
XX      between tumour and normal cells and which has cytostatic activity. (I)
XX      work as modulators of Ras activity by inducing expression of tumour
XX      suppressor genes. (I), and polypeptides encoded by them, are useful as
XX      targets for diagnosis or therapy and in screening to determine the
XX      effects of an active compound (potential pharmaceutical) on a cell line,
XX      particularly for diagnosis and treatment of tumors, especially by
XX      modulating expression of (I) (by gene therapy, antisense RNA or ribozyme
XX      methods) or by modulating the amount and/or location of (I)-encoded
XX      polypeptides (by administration of the polypeptide or its activator,

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CC antibody (optionally as a conjugate) or inhibitor). The method allows  
 CC identification of many Class II tumour suppressor genes (i.e., genes that  
 CC are not primary targets for tumour-initiating mutations). AAH8192-  
 CC AAH8236 represent the human and rat derived nucleic acid fragments  
 CC described in the method of the invention

XX SQ Sequence 4231 BP; 1170 A; 895 C; 1015 G; 1151 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
0	6779.00	4231	1323	1	1	0	0
Best Local Similarity:	99.98						
Query Match:	99.98						
DB:	5						

US-09-976-858-42 (1-1325) x AAH81778 (1-4231)

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QY      1 MetLeuProValTyrGlnGluValIySProAsnProLeuGlnAspAlaBsnLeuCySer 20
DB      116 ATGCTGCCCGTGTACAGAGAGGTGAAGCCAAACCGCTGCAGAGCGCAACATCTGTCA 175
QY      21 ArgValPhePheTTPTrLeuBsnProLeuBsnPheIySILeGlyHISLyArgPrgLeuGlu 40
DB      176 CGCGTCTCTCTGTGGCTCAATCCCTGTTTAAATGGCCATTAACGGAGATTAGAG 235
QY      41 GluAspAspMetTyrSerValLeuProGluBpArgSerGlnHISLeuGlyGluGluLeu 60
DB      236 GAAAGATGATATATATTCAGTGTGTCAGAGAGCCGCTCAGACACCTTGAGAGAGATTG 295
QY      61 GlnGlyPheTTPAspLySGIuValLeuArgAlaGluAsnAspAlaGlnLyBProSerLeu 80
DB      296 CAAGGTTCTGGATTAAGAAAGTTTAAAGCTGAGAAATGACGACAGACAGACGCTTCTTA 355
QY      81 ThrArgAlaIleIleIySGyethrTrpLySerTyrLeuValLeuGlyIlePheThrIleu 100
DB      356 ACAAAGACATATTAAGTGTACTGGAATTTATTTAGTTTGGAAATTTTACGTTA 415
QY      101 IlegGluSerAlaIyValIleGlnProIlePheLeuGlyIySILeAsnTyrPhe 120
DB      416 ATTGAGAAAGTGCCTCAAGTAAATCCAGCCCATTTTGGGAAATTAATTAATTTT 475
QY      121 GluAsnTyrAspProMetAspSerValAlaIeAsnThrAlaTyrAlaThrVal 140
DB      476 GAAATTTATGATCCCATGATCTGTGCTTGAACACAGCGTACGCCATCCACGGTG 535
QY      141 LeuThrPheCyethrLeuIleuAlaIleuHISISLeuTyrPheTyrHISValGln 160
DB      536 CTGACTTTTTCAGCGCTCATTTTGGCTTACGTCACTTAATTTTATCATCGTTGAG 595
QY      161 CysAlaGlyMeTArgLeuArgValAlaMeTcySHISMeTILeTyrArgIySAlaLeuArg 180
DB      596 TTGCTGGGATAGGTTACGAGTACGATGCTCCATATGATTTTACGAAAGCATTGCT 655
QY      181 LeuSerAsnMeTAlaMeTGLySerThrThrTrhTrhGlyGlnIleValAsnLeuSerAsn 200
DB      656 CTTAGTAACATGCGCATGGGGAAGAACCAACAGAGCCAGATGTCATTCGTCGCAAT 715
QY      201 AspValAsnLyPheAspGlnValThrValPheIySHISLeuPheLeuThrAlaGlyProLeu 220
DB      716 GATGTGAACAAATTTGATCAGGTGACAGTGTCTTACACTTCTGTTGGGCAAGACACTG 775
QY      221 GlnAlaIleAlaValThrAlaLeuLeuTTPMeTGLuIleGlyIleSerCySLeuAlaGly 240
DB      776 CAGGCGATGACGTACATCCCTACTCTGAGATGAGATAGAAATTCGTCGTTGTTGG 835
QY      241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCySphGlyLyLeuPheSerSer 260
DB      836 ATGGAGTTCTATATCTTCTCCGCTTGAAGCGTGTTTGGGAAGTTGTTTCATCA 895
QY      261 LeuArgSerLyThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280
DB      896 CTGAGAGATTAACCTGCACTTTCACGAGTGCAGAGATCAGACCATGATGAAGTTATA 955

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QY 281 ThrGlyIleArgIleIleIleYserThrAlaTPGluLysSerPheSerAsnLeuIleThr 300  
 DB 956 ACTGATTAAGAGTAATATAAATATGACGCTGGAAAAAGTCATTTTCAATCTTATTACC 1015  
 QY 301 AsnLeuArgLysLeuIleSerLysIleLeuArgSerCysLeuArgIleMetAsn 320  
 DB 1016 AATTGAGAAAGAGAGATTTCCAAAGATTCTGAGAAAGTTCTGCTCAGGGGAGTAAGAT 1075  
 QY 321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrVal 340  
 DB 1076 TTGGCTTCGTTTTCAGTGCAAGCAAAATCATGCTGTTGTGACCTTCCACCTACCGTG 1135  
 QY 341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuThrVal 360  
 DB 1136 CTCCTCCGAGTGTATCATACAGCCGCGTGTGTCGAGTGAAGCTGTATGGAGCT 1195  
 QY 361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAla 380  
 DB 1196 GTGGCGCTGACGGTTACCTCTTCTTCCCTCAGCATTTGAGAGGGGTGCAGAGGCAATC 1255  
 QY 381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400  
 DB 1256 GTCAACATCCGAAAGATCCAGACTTTTGTCTATGATGAGATATCAAGCGCAACCGT 1315  
 QY 401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheThrPhe 420  
 DB 1316 CAGCTCCGCTCAGATGAGTAAGTAAGTGCATGTCAGAGATTTCATGCTTTTGGAGT 1375  
 QY 421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440  
 DB 1376 AAGGATCAGAGACCCCAACTCTACAGGCCCTTCTTACTGTCAAGCTGCCAATTG 1435  
 QY 441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460  
 DB 1436 TTAGCTGTGTCGCGCCCGTGGAGCAGGAAAGTCATCATCTTAAGTCCGCTCGCGG 1495  
 QY 461 GlnLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaIleThrAlaSerGln 480  
 DB 1496 GAATGGCCCCCAAGTCAAGGCGCTGGTCACCGTGCATGAGAAATGCTTATGTCTCAG 1555  
 QY 481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysIleThrGln 500  
 DB 1556 CAGCCCTGGGTTCTTCGGGAATCTGAGAGATTAATTTTATTTGGGAAGAAATATGA 1615  
 QY 501 LysGluArgTrpGluLysValIleLysValaCysAlaLeuLysLysAspLeuLeuLeu 520  
 DB 1616 AAGGAACGATAGAAAAAGTCATAAAGGCTGTGCTGAAAAAGATTTCACGCTGTG 1675  
 QY 521 GlnAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540  
 DB 1676 GAGGATGGGATCTGATCTGTAGTAGAGATTCGGGAAACCAAGCTGATGAGAGGAGAA 1735  
 QY 541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560  
 DB 1736 GACAGGGTAAACCTTCGAAAGACAGTGTATCAAGATGCTGACATCTATCTCTGACAT 1795  
 QY 561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGln 580  
 DB 1796 CCTCTCAGTGCAGTATGACGGAAGTTAGCAGACACTGTTGCACTGTGATTTGTCA 1855  
 QY 581 IleLeuHisGluLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600  
 DB 1856 AATTGGACAGAAATCAACAATTTTAGACTCATACGTTGACAGTACTCAAACTGCA 1915  
 QY 601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620  
 DB 1916 AGTCAGATTCTGATTTGAAAGATGCTAAGATGCTGACAGAGGAGCTTACCTAGTTC 1975  
 QY 621 LeuLysSerGlyTyrLeuAspPheGlySerLeuLeuLysLysAspAsnGlnIleSerGln 640  
 DB 1976 CTAATAATCTGATATGATTTTGGCTCCCTTTAAAGAGATTAAGAGAAAGTGAACA 2035

QY 641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGlySerSerValTrp 660  
 DB 2036 CCTCAGATTCCAGAACTCCACACTTAAGATCTTACTTACAGAGCTTCGGTTGG 2095  
 QY 661 SerGlnIleSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGln 680  
 DB 2096 TCTCAACAATCTTTCAGACCCCTCTGAAAGATGTGCTCTGAGAGCCAAATACAGAG 2155  
 QY 681 AsnValProValThrLeuSerGluLysLeuAspSerGluLysValGlyPheGlnAla 700  
 DB 2156 AATGTCCAGATTACATCATCAGAGAGAACCGTCTGAAAGAAAGTGGTTTTCAGGCC 2215  
 QY 701 TyrLysAsnTyrPheArgAlaGlyAlaHisIleTrpIleValPheIlePheLeuIleLeuLeu 720  
 DB 2216 TTTAAGATTAATTCTAGAGCTGTGTCTCATCTGATGTTCTTCAATTTCTTCTCCTA 2275  
 QY 721 AsnThrAlaAlaGlnValAlaIleTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740  
 DB 2276 AACACTGACGCTCAGGTTGCTCATGTGCTTCAMAAGTTGGTGCTTTCATACAGGCCAATC 2335  
 QY 741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyLysAsnValThrGluLysLeuAsp 760  
 DB 2336 AAACAAGATATGCTAAATGTCACTGTAAATGAGAGAGAAATGTAAACGAGAACTAGAT 2395  
 QY 761 LeuAsnTrpTyrLeuGlyTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780  
 DB 2396 CTTAACTGTACTTGAATTTATTTACGTTTAACTGTAGTACCTGTTCTTTTGGCAT 2455  
 QY 781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800  
 DB 2456 GCAAGATCTCTATGATGTATTCAGTCCCTGTGTAATCTTTCACAAACTTGCACAAACAA 2515  
 QY 801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820  
 DB 2516 ATGTTTGAATCAATCTGAAAGCTCCGGTATTAATCTTTGATGAAGAAATCCATAGAGAA 2575  
 QY 821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840  
 DB 2576 ATTTTTAATCGTTTCTCCAAAGACATTGACACTTGATGATTTCTGCCCTGACGTTT 2635  
 QY 841 LeuAspPheIleGlnThrLeuLeuGlnValGlyValAlaSerValAlaValAlaVal 860  
 DB 2636 TTAGATTTCACTCAGACATTGCTACAGTGTGTGTGTGTCTGTGGCTGTGGCCGG 2695  
 QY 861 IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880  
 DB 2696 ATTTCTTGATCGCAATACCTTGTGTTCCCTTGGAAATCATTTTCAATTTTCTTGGCGA 2755  
 QY 881 TyrPheLeuGluThrSerArgAspValLysArgLeuGlnIleThrArgSerProVal 900  
 DB 2756 TATTTTGGAAACGTCAAGAGATGTGAAGCGCTGGAATCTTCAACTCGAGTCCAGTG 2815  
 QY 901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpTrpIleArgAlaTyrLysAlaGln 920  
 DB 2816 TTTTCCCACTGTATCTTCTCTCCAGGGGCTGTGACATCCGGGACATCAACACAGAA 2875  
 QY 921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGlnAlaTrpPheLeu 940  
 DB 2876 GAGAGTGTCAAGAACTGTTGATGACACACAGAGATTTCATTCAGAGGCTGTGTTCTTG 2935  
 QY 941 PheLeuThrTrpSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960  
 DB 2936 TTTTGGACAGTCCCGCTGGTGTGCGCTCGCTGGAAGCCATCTGAGCAATGTTGTC 2995  
 QY 961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980  
 DB 2996 ATCACTGTTGCTTTGGTTCCTGATTTCTGGCAAAAATCTGGAAGCGGGAGGTTGGT 3055  
 QY 981 LeuAlaLeuSerTyrAlaLeuThrLeuMetCylMetPheGlnTrpCysValArgGlnSer 1000  
 DB 3056 TTGGCACTGTCTTAATGCTCAGCTCATGTGGGAGATGTTTCAGTGTGTGTTGCAAAAGT 3115  
 QY 1001 AlaGluValGluAsnMetMetIleSerValGluTrpValIleGluTyrThrAspLeuGlu 1020

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DB 3116 GCTGAAGTGGAGAAATATGATGATCTCAGTAGAGAAAGGGTCATGAAATACACACACCTTGAA 3175
QY 1021 LysGluAlaProThrGluTyrGlnIleuysAspPropProAlaTTrpProHisGluGlyVal 1040
DB 3176 AAAGAAAGCACTGGGAAATATACGAAACCCCAACCAAGCCCTGGCCCATAGAGAGAG 3235
QY 1041 IleIlePheAspAsnValAsnPhemetySerProGlyGlyProleuValIleuysHis 1060
DB 3236 ATATCTTTGACAAATGTGAATCTTCATGTACAGTCCAGGCGGGCTCTGTTACTGAAGCAT 3295
QY 1061 LeuThrAlaLeuIleLysSerGlnGlyValGlyLeuValGlyValArgThrGlyValGly 1080
DB 3296 CTGACAGCACTCATTAATCAACAGAAAGTTGGCATTTGGGAAAGAACCCGAGCTGGA 3355
QY 1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyValIleTrrpIle 1100
DB 3356 AAAAGTTCCTCATCTCAGCCCTTTTATGATGTCCAGAACCCGAGGTAAATTTGGATT 3415
QY 1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysMetSerIleIle 1120
DB 3416 GATTAAGATCTTGACAACTGAATTTGACTTCACGATTTAAGAGAAATGTCAATCATA 3475
QY 1121 ProGlnGluProValIleuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
DB 3476 CCTCAGGAACCTGTTTGTTCCTCAGGAACATGAGAAACCTGGATCCCTTTAAGAG 3535
QY 1141 HisThrAspGluGluLeuThrAsnAlaLeuGlnGlyValGluLeuIleGluThrIleGlu 1160
DB 3536 CACACGAGTAGAGAACTGTGGAATGCTTACAGAGGTACCACTTAAACCAATTTGA 3595
QY 1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheserValGly 1180
DB 3596 GATCTTCCCTCGTAAATGTGATCTGAATTAAGCAGATTCAGATTCATTTTGTGTGA 3655
QY 1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200
DB 3656 CAAAGCAACTGGTGTGCTTCGCAAGGCAATTTCTCAGGAAATCAGATATTGATTAT 3715
QY 1201 AspGluAlaThrAlaAsnValAspProArgThrAspGlnLeuIleGlnLysIleLeuArg 1220
DB 3716 GATGAAGCAACGCGCAATGTGATCCAGAACCTGAAGTATTAATCAAAAAAATCCGG 3775
QY 1221 GlnLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
DB 3776 GAGAAATTTGCCCATCGACACCGTGTACCATTTGACACAGANTGAAACCATTTATGAC 3835
QY 1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260
DB 3836 ACGCAACAAGATATATGTTTATGATTACAGAAAGCATGAAGAATATGATGAGCCGTATGTT 3895
QY 1261 LeuLeuGlnAsnLysGlnSerLeuPheTyrLysMetValGlnGlnLeuLysAlaGlu 1280
DB 3896 TTGCTGCAAAATTAAGAGCCCTATTTTTCAAGATGTGTCAACACTGGGCAAGGAGAA 3955
QY 1281 AlaAlaAlaLeuThrGlnThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300
DB 3956 GCCGCTGCCCTCAGTGAACAGCAAAACAGTATATTCTTCAAAAGAAATTTTCCACATATT 4015
QY 1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
DB 4016 GGTCACTACAGCAACATGTGTTACAAACACTTCCATGAGACAGCCCTGACCTTAATATT 4075
QY 1321 PheGluThrAlaLeu 1325
DB 4076 TTCGAGACAGCACTG 4090

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RESULT 10
ABV75072
ID ABV75072 standard; DNA; 4231 BP.
XX
AC ABV75072;
XX

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DT 19-FEB-2003 (first entry)
XX
DE Human DevG4 homologue protein encoding DNA.
XX
KW Protein disulfide isomerase; DevG20; ABC transporter; DevG4; DevG22;
KW anorectic; immunomodulator; antidepressant; antidiabetic; hypotensive;
KW antitartaric; antileukemic; antilipemic; osteopathic; antilathritic; gene;
KW litholytic; hepatotropic; cyostatic; neuroprotective; gene therapy;
KW transgenic; human; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 115..4092
FT /tag=a
FT /product="DevG4 homologue protein"
XX
PN WO200279238-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002MO-BP003540.
XX
PR 02-APR-2001; 2001EP-00108315.
PR 01-JUN-2001; 2001EP-00113419.
XX
PA (DEV4-) DEVELOPMENTAL BIOLOGICALS FORSCH.
XX
PI Eulenberger K, Bremer G, Ciossek T, Haeder T, Steuernagel A;
XX WPI; 2003-067420/06.
XX P-PsDB; ABB82645.
DR
XX
PT New protein disulfide isomerase and ABC transporter nucleic acids or
PT polypeptides, useful for diagnosing, treating or preventing obesity,
PT hypertension, heart disease, hypercholesterolemia, osteoarthritis,
PT gallstones or cancer.
XX
PS Claim 2; Fig 9C; 99p; English.
XX
CC The invention relates to pharmaceutical composition comprising carrier,
CC diluents and/or adjuvants, with any of: (a) a nucleic acid molecule of
CC the protein disulfide isomerase (DevG20) or ABC transporter (DevG4 or
CC DevG22) gene family; (b) a polypeptide encoded by (a); (c) a fragment or
CC variant of (a) or (b); or (d) an antibody, an aptamer or another receptor
CC recognizing (a) or (b). The composition is useful for manufacturing an
CC agent for detecting and/or verifying, diagnosing, treating, alleviating
CC or preventing a metabolic disorder, e.g. obesity, adipositas, eating/body
CC weight disorders, cachexia (wasting), pancreatic dysfunction (diabetes
CC mellitus), hypertension, arteriosclerosis, coronary artery disease (CAD),
CC coronary heart disease, hypercholesterolemia, dyslipidemia,
CC osteoarthritis, gallstones, cancer (cancer of the reproductive organs),
CC sleep apnea, disorders related to ROS production and neurodegenerative
CC diseases in cells, cell masses, organs and/or subjects. The inhibitors,
CC modulators or agents identified above are useful for treating, preventing
CC or alleviating the diseases mentioned. The nucleic acid molecule of
CC DevG20, DevG4 and/or Dev is also useful for preparing a non-human animal
CC which over- or underexpresses the DevG20, DevG4 and/or Dev gene product.
CC The present sequence represents a DNA encoding a human DevG4 homologue
CC protein, a ATP-binding cassette, sub family C (CFTR/MRP), member 4, also
CC referred to as ABC4 and MPR4 (Gen Bank Accn No. NM_005845)
XX
SQ Sequence 4231 BP; 1170 A; 894 C; 1016 G; 1151 T; 0 U; 0 Other;

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Alignment Scores:
Pred. No.: 0
Score: 6779.00
Percent Similarity: 99.9%
Best Local Similarity: 99.8%
Query Match: 99.9%
DB: 8
Length: 4231
Matches: 1323
Conservative: 1
Mismatch: 1
Indels: 0
Gaps: 0

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US-09-976-858-42 (1-1325) x ABV75072 (1-4231)

QY 1 MetLeuProValIYrGInGIuValIySProAsnProLeuGlnAspAlaAsnLeuCySer 20  
 DB 116 ATGCTGCCGTGTAACAAGAGGTGAAGCCCAACCCGCTCAAGACCGCAACCTGCTCA 175  
 QY 21 ArgValPhePheTrpIleuAsnProLeuPheIyIleGIyHlSlySArgIleuGln 40  
 DB 176 CCGGTGCTCTTGGGGCTCAATCCCTGTTTAAATTGGCCATTAACGAGATTAAGAG 235  
 QY 41 GluAspAspMetTySserValLeuProGluAspArgSerGlnHlSleuGIyGluLeu 60  
 DB 236 GAAAGATGATATGATTCAGTGTCTGCCAAGAACCGCTCAACACCTTGAGAGGGAGTGG 295  
 QY 61 GInGIyPheTrpAspIySgluValIleuAspAlaGluAsnAspAlaGlnIySProSerLeu 80  
 DB 236 CAAGGCTTGGGATTAAGAAAGTTTAAAGCTGAAGATGACGACAGAACCTTCTTTA 355  
 QY 81 ThrArgAlaIleIleIySCTyTrpIySserTyLeuValIleuGIyIlePheThrLeu 100  
 DB 356 ACAAGAGCAATCATAAAGTGTACTGGAATCTTATTAGTTTGGGAATTTTACGTTA 415  
 QY 101 IlegIuIuSerAlaIySValIleGlnProIlePheLeuGIyIySleIleAsnTyPhe 120  
 DB 416 ATTTGAGAAAGTGCACAAAGTAAATCCAGCCCATATTTTGGGAAAATTTATTAATTTT 475  
 QY 121 GluAsnTyAspProMetAspSerValAlaIleuAsnThrAlaTyAlaIyAlaThrVal 140  
 DB 476 GAAATTTATGATCCCATGGATTTCTGTGCTTGAACACAGCGTACCCCTATGCAAGG 535  
 QY 141 LeuThrPheCySThrLeuIleIleuAlaIleuHlSleuTyPheTyHlSValGln 160  
 DB 536 CTGACCTTTTGGACGCTCATTTTGGCTATACGCAATCACTTAATTTTATCACGTTG 595  
 QY 161 CySAlaGIyMeCArgLeuArgValAlaMetCySHlSmetIleTyArgIyAlaLeuArg 180  
 DB 596 TGTGTGGGATGAGGTACAGATGACATGTCACATATGATTTATCGAAGCACCTTCCT 655  
 QY 181 LeuSerAsnMetAlaMeCglYlySerThrThrGlnIleValAsnLeuSerAsn 200  
 DB 656 CTTTATGATACATGCAATGGGGAAGACACACAGGCAAGTACATGCTGCTGCAT 715  
 QY 201 AspValAsnIySAspAspGlnValThrValPheLeuHlSleuThrAlaGIyProLeu 220  
 DB 716 GATGGAACAATTTGATCAGGTGACAGTCTTACACTTCTGTGGGACAGACACAG 775  
 QY 221 GlnAlaIleAlaValThrAlaLeuLeuTyPMeCgluIleGIyIleSCTySleuAlaGIy 240  
 DB 776 CAGGCGATCGCAGTACGCTGCTGATGAGATGAGAAATACGCTGCTGCTGG 835  
 QY 241 MetAlaValIleuIleIleuLeuProLeuGlnSerCySPhGIyIyIleuPheSerSer 260  
 DB 836 ATGGCAGTCTTATCATCTGCTGCTGCTGCAAGCTGTTTGGGAAGTGTCTCATCA 895  
 QY 261 LeuArgSerTySThrAlaThrPheThrAspAlaArgIleArgThrMeCAsnGluValIle 280  
 DB 896 CTGAGAGAGTAAACGCACTTCAACGATGCAAGATCAAGACCATGAATGAAGTATA 955  
 QY 281 ThrGIyIleArgIleIleIySmetTyAlaIyPGLuIySCTySAsnLeuIleThr 300  
 DB 956 ACTGTATTAAGATATATAAAATGTACGCTGGGAAAAGTCAATTTCAATCTTATACC 1015  
 QY 301 AsnLeuArgIyIySgluIleSCTySleuAspSerCySLeuArgIyIyMeCAsn 320  
 DB 1016 AATTTGAGAAAGAGAGATTTCCAAAGATTCGAAGAGTCTGCTGCTGAGGAGATGAAT 1075  
 QY 321 LeuAlaSerPhePheSerAlaSerIySleIleValPheValThrPheThrTyAla 340  
 DB 1076 TTGGCTGCTGTTTTCAGTGAAGCAAAATCATCGTGTGATCACTTCAACCTACG 1135  
 QY 341 LeuLeuGIySerValIleThrAlaSerArgValPheValAlaValThrLeuTyAla 360  
 DB 1136 CTCCTCGGAGTGTATCACACGACCGCTGTGCTGAGTGAAGCTGTATGAGGCT 1195

QY 361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGlnAlaIle 380  
 DB 1196 GTGGCGGTGACGGTTACCTCTTCTCCCTCAAGCATTTGAGAGGCTGTCAAGAGCAATC 1255  
 QY 381 ValSerIleArgArgIleGlnThrPheLeuLeuAspGluIleSerGlnArgAsnArg 400  
 DB 1256 GTCAACATCCGAAGATCCAGACCTTTTGGCTACTGTATGAGATATCACAGCGCAACCGT 1315  
 QY 401 GlnLeuProSerAspGIyIySlySmetValHlSValGlnAspPheThrAlaPheTrpAsp 420  
 DB 1316 CAGCTGCCGTCAAGATGTAAAGATGTGATGTCAGAGATTTTACGCTTTTGGGAT 1375  
 QY 421 IySAlaSerGIyIySProThrLeuGlnIyIleuSerPheThrValArgProGIyGluLeu 440  
 DB 1376 AAGGATCAAGAACCCCACTCATCAAGGCTTCTTACGTGACAGCTGCGCAATTG 1435  
 QY 441 LeuAlaValIyGIyProValIyAlaGIyIySCTySserSerLeuLeuSerAlaValIleuGIy 460  
 DB 1436 TTAGCTGTGTGCGCCCGTGGAGCAGGAAAGTCACTGTTAAGTGCCTGCTCGGG 1495  
 QY 461 GluLeuAlaProSerHlSgluValSerValHlSgluArgIleAlaTyAlaSerGln 480  
 DB 1496 GAATTTGCCCCAAGTCAAGGCTGTGTCAGCTGATGGAAGAAATGCTATGTCTCG 1555  
 QY 481 GlnProTPValPheSerGIyThrLeuArgSerAsnIleLeuPheGIyIySlySArgIu 500  
 DB 1556 CAGCCTGGGTGTTCTCGGAACCTTGAGAGTAAATTTTATTTGGGAAGAAATTTGA 1615  
 QY 501 IySgluArgTyGIyIySValIleIySAlaCySAlaLeuIySlySAspLeuGlnLeu 520  
 DB 1616 AAGGAACATATGAAGAAAGTCAATAAGCTTGTGCTGAAAAGATTTACAGCTGTG 1675  
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 QY 541 AlaArgValAsnLeuAlaArgAlaValTyGlnAspAlaAspIleTyLeuLeuAspAsp 560  
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 DB 1796 CCTTCAGTGCAGTATGATGCGGAAGTGTAGCAGACCTTGTCAACTGTGATTTGTCA 1855  
 QY 581 IleLeuHlSgluIySleIleThrIleuValThrHlSglnLeuGlnTyIleuValAla 600  
 DB 1856 ATTTGCAATGAGAGATCACAATTTTATGATCTATCACTGACAGTACCTCAACCTGCA 1915  
 QY 601 SerGlnIleuIleIleuIySAspGIyIySmetValGlnIySgluTyThrTyThrGluPhe 620  
 DB 1916 ACTCAGATTTGATATTTAAGATGTGTAAATGTGTGCAAGAGGGAATTTACCTAGTTC 1975  
 QY 621 LeuIySserGIyIleAspPheGIySerLeuLeuIySlySAspAsnGluIuSerGluGln 640  
 DB 1976 CTAATAATCTGGATATGATTTTGGCTCCCTTTTAAAGAGATTAATGAGAAAGTGAACA 2035  
 QY 641 ProProValProGIyIySProThrLeuArgAsnArgThrPheSerGluSerSerValTrp 660  
 DB 2036 CCTCCAGTTCCAGGAACCTCCCACTAAAGATGCTACCTTCTCAGAGCTTCGCTTGG 2095  
 QY 661 SerGlnIuSerSerArgProSerLeuIySAspGIyAlaLeuGluSerGlnAspThrGlu 680  
 DB 2096 TCTCAACATCTTCTAGACCTCTCTTGAAGATGTGTCTGAGAGGCCAAGATCAAG 2155  
 QY 681 AsnValProValThrLeuSerGluIuAsnArgSerGIyIySValGIyPheGlnAla 700  
 DB 2156 AATGCTCCAGTTATCACTATCAAGAGAACCGTCTGAAAGAAAGTGTTCAGAGCC 2215  
 QY 701 TyTrpAsnTyTrpPheArgAlaGIyAlaHlSTrpIleValPheIlePheLeuIleuLeu 720  
 DB 2216 TATAAGATTTACTCAGAGCTGTGCTCACTGATGTCTTCATATTTCTTATCTCTTA 2275  
 QY 721 AsnThrAlaIleGlnValAlaIyTyValLeuGlnAspTrpTrpLeuSerTyTrpAlaAsn 740

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Db      2276 AACACGTGACGCTCAGGTTGCCATGCTTCAAGATTGGTGGCTTTCATACAGGCGGAAC 2335
Qy      741  LysGlnSerMetLeuAsnValThrValAsnGlyGlyValAsnValThrGlnLysLeuAsp 760
Db      2336 AACAAGATGCTTAATATCTCACTGAATGAGGAGAAATGTAAACCAAGAGCTAGAT 2395
Qy      761  LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780
Db      2396 CTTAATCTGCTAGTGAATTTATTCAGGTTTAACGTAGCTACGTTCTTTTGGCATA 2455
Qy      781  AlaAspSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800
Db      2456 GCAAGATCTCTATTGGTATTCTACGCTCTGTTAACTCTTCACAAACTTGCACAAACAA 2515
Qy      801  MetPheGlnSerIleLeuLysValProValLeuPhePheAspAspAsnProIleGlyArg 820
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Qy      821  IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840
Db      2576 ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTGCTGCGCTGACGTTT 2635
Qy      841  LeuAspPheIleGlnThrLeuLeuGlnValGlyValValSerValAlaValAlaVal 860
Db      2636 TTAGATTTTCATCCAGACATTGCTACAAAGGTGGTGGTGGTCTCTGTGCTGTGGCCG 2695
Qy      861  IleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880
Db      2696 ATTTCTTGAATCGCAATACCTTGGTTCCTCCCTTGGAAATCTTCAATTTTCTTGGGCA 2755
Qy      881  TyrPheLeuGlnThrSerArgAspValLysArgLeuGlnSerThrThrArgSerProVal 900
Db      2756 TATTTTGGAAACGTCAGAGATGTGAAGCGCTCGAAATCTACCACTCGAGTCCAGTG 2815
Qy      901  PheSerHisLeuSerSerSerLeuGlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlu 920
Db      2816 TTTTCCCATCTGTCATCTTCTCCAGGGGCTCTGACACATCCGGCAATACAAAGACAGA 2875
Qy      921  GluArgCysGlnGlnLeuPheAspAlaHisGlnAspLeuHisSerGlnAlaTrpPheLeu 940
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Qy      941  PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960
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Qy      961  IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980
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Qy      3116 GCTGAAGTTGAGAAATATGATGATCTCAGTAGAAAGGTCATTAATACAGACCTTGA 3175
Db      1021 LysGlnAlaProTrpGlnTyrGlnLysArgProProProAlaTrpProHisGlnGlyVal 1040
Qy      3176 AAGAAGACACTTGGGAAATATCAAGAAACGCCACACAGCCCTGGCCCATGAAAGAGTG 3235
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Qy      3236 ATATATCTTGAACATGTGAATTCATGATACAGTCCAGGTGGGCTCTGTGATCTGAAGCAT 3295
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Qy      3296 CTGACGACACTATTAATCAACAAGAAAGTTGGGATTTGGGAAAGAACCGGAGCTGGA 3355
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Db      3356 AAAAGTCCCTCAGCTCAGCCCTTTTAGATTGTCAGAACCCGGAAGTAAAAATTGCA 3415
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Db      3416 GATTAAGATCTTGACACACTGAAATTTGCACTTACAGATTTTAAGGAAGAAATGTCATATA 3475
Qy      1121 ProGlnLysProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140
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Qy      1141 HisThrAspGlnGlnLeuTrpAsnAlaLeuGlnGlnValGlnLysLeuGlyThrIleGln 1160
Db      3536 CACACGAGATGAGAACTGTGAGATGCTTACAGAGGTACACTTAAGAAACCACTTGA 3595
Qy      1161 AspLeuProGlyLysMetAspThrGlnLeuAlaGlnSerGlySerAsnPheSerValGly 1180
Db      3596 GATCTTCTGTGAAATGATGATATGCAATTAAGAGATCAGATTCGAATTTTAGTGTGA 3655
Qy      1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuAlaGlyLysAsnGlnIleLeuIleIle 1200
Db      3656 CAAGACAACTGTGTGCTTGGCCAGGCAATTCACAGAAAAATCAGATATGTATAT 3715
Qy      1201 AspGlnAlaThrAlaAsnValAspProArgThrAspGlnLeuIleGlnLysLysIleArg 1220
Db      3716 GATGAAGGACGCGCAATGTGATCAGAACTGATGATCTTAATCAAAAAAATCCGG 3775
Qy      1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleLeuAsp 1240
Db      3776 GAGAAATTTGGCCCATCTGACCGGTCTTACATTCGACACAGATTAACCATTTATGAC 3835
Qy      1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGlnTyrArgGlnProTyrVal 1260
Db      3836 AGCGACAAGATATGTTTGTGATTCAGAGAACCTGAAAGAAATAGAGAGCCGATATTT 3895
Qy      1261 LeuLeuGlnAsnLysGlnSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280
Db      3896 TTGCTGCAAAATTAAGAGAGCTATTTTACAGATGAGTGACACACTGGCAGGCAAGAA 3955
Qy      3956 GCCGCTGCCCTCAGCAAGCAAGCAAGCAAGATATCTTCAAAAGAAATTAATCCACATAT 4015
Db      1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320
Qy      4016 GGTCACTACGACCAACATGTTTACAAACACTTCCATGACAGCCCTCAACCTTAATACT 4075
Db      1321 PheGlnThrAlaLeu 1325
Qy      4076 TTCGAGACGACCTG 4090

```

RESULT 11  
 ADN39253  
 ID ADN39253 strand; cDNA; 4231 BP.  
 AC ADN39253;  
 XX 17-JUN-2004 (first entry)  
 DT  
 DE Cancer; angiogenesis; fibrosis-related nucleic acid, SEQ ID NO:571.  
 XX Human; differential expression; cancer; angiogenic disorder;  
 XX fibrotic disorder; psoriasis; ischemia; heart disease; atherosclerosis;  
 XX inflammatory disease; autoimmune disease;  
 KW retinal neovascularization syndrome; scarring; uterine fibroid;  
 KW detection; diagnosis; prognosis; drug screening; drug targeting;  
 KW wound healing; contraception; cytostatic; cardiac; immunomodulatory;  
 KW vulnery; gene therapy; vaccine; gene; ss.  
 OS Homo sapiens.  
 XX  
 OS  
 XX  
 PN WO2003042661-A2.  
 XX  
 PD 22-MAY-2003.

XX 13-NOV-2002; 2002MO-US036810.  
PF 13-NOV-2001; 2001US-0350666P.  
XX 21-NOV-2001; 2001US-0332464P.  
PR 29-NOV-2001; 2001US-0334393P.  
PR 03-DEC-2001; 2001US-0335394P.  
PR 14-DEC-2001; 2001US-0340376P.  
PR 08-JAN-2002; 2002US-0347211P.  
PR 10-JAN-2002; 2002US-0347349P.  
PR 08-FEB-2002; 2002US-0355250P.  
PR 13-FEB-2002; 2002US-0356714P.  
PR 20-FEB-2002; 2002US-0359077P.  
PR 29-MAR-2002; 2002US-0368099P.  
PR 04-APR-2002; 2002US-0370110P.  
PR 12-APR-2002; 2002US-0372246P.  
PR 05-JUN-2002; 2002US-0386614P.  
PR 16-JUL-2002; 2002US-0396839P.  
PR 22-JUL-2002; 2002US-0397775P.  
PR 22-JUL-2002; 2002US-0397845P.  
PR 09-SEP-2002; 2002US-0409450P.  
XX (BOSB-) EOS BIOTECHNOLOGY INC.  
XX Afar D, Aziz N, Gineburg WM, Gish KC, Glynn R, Hevizi PA;  
PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnick A;  
XX WPI; 2003-468649/44.  
DR P-PSDB; ADN39254.  
XX Determining the presence or absence of a pathological cell in a patient,  
PT useful for diagnosing, prognosing or treating cancer, comprises detecting  
PT a nucleic acid in a biological sample.  
XX Claim 8; SEQ ID NO 571; 1385pp; English.  
XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064)  
CC whose expression is upregulated or downregulated in specific cancers or  
CC other diseases such as angiogenic or fibrotic disorders, and to methods  
CC of determining the presence or absence of a pathological cell in a  
CC patient by detecting a nucleic acid at least 80% identical to those of  
CC the invention or by detecting a polypeptide of the invention. The  
CC invention also relates to expression vectors and host cells comprising a  
CC nucleic acid of the invention; antibodies which specifically bind a  
CC polypeptide of the invention; use of such antibodies for drug targeting;  
CC and methods of screening for modulators of activity or expression of the  
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,  
CC antibodies and methods are useful for diagnosing, prognosing and treating  
CC cancer and other conditions such as psoriasis, ischemia, heart disease,  
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal  
CC neovascularization syndromes, scarring and uterine fibroids. They may  
CC also be useful in wound healing and in contraception. The present  
CC sequence represents a nucleic acid sequence of the invention.  
XX SQ Sequence 4231 BP; 1170 A; 895 C; 1015 G; 1151 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 0 Length: 4231  
Score: 6779.00 Matches: 1323  
Percent Similarity: 99.9% Conservative: 1  
Best Local Similarity: 99.8% Mismatches: 1  
Query Match: 99.9% Indels: 0  
DB: 11 Gaps: 0  
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QY 1 MetLeuProValTyrGlnGluValIlePheProAsnProLeuGlnAspAlaAsnLeuCysSer 20  
DB 116 ATGCTGCGCCGCTTACAGAGAGGTGAAGCCCAACCGCTGACAGAGCCGCAACATCTGCTCA 175  
QY 21 ArgValPhePheTrpTrpLeuAsnProLeuPheValIleGlyHisIleValArgArgLeuGlu 40  
DB 176 CCGGCTTCTTCTGCGTCAATCCCTTGTAAATGATGGCATTAAGAGATTAAAG 235

QY 41 GluAspAspMetCysSerValLeuProGluAspArgSerGlnHisLeuGlyValGluLeu 60  
DB 236 GAGATGATATGATATTCAGTCTGCTGCCAGAGAGCCCTCAGACGACCTTGAGAGAGATTG 295  
QY 61 GlnGlyPheTrpAspPheGluValLeuArgAlaGluAsnAspAlaGlnIlePheProSerLeu 80  
DB 236 CAGGCTTCTGAGATTAAGAAAGTTTAAAGACTGAGATGAGACAGACAGGCTTCTTAA 355  
QY 81 ThrArgAlaIleIleIleValCysTyrTrpPheSerTyrLeuValLeuGlyIlePheThrLeu 100  
DB 356 ACAAGAGCAATCATTAAGTGTACAGAAATCTTATTTAGTTTGGGAATTTTAACTGTA 415  
QY 101 IleGluGluSerAlaValValIleGlnProIlePheLeuGlyValIleIleAsnTyrPhe 120  
DB 416 ATGAGGAAAGGCCAAAGTATCCAGCCCATTTTGGGAAATTAATTAATTAATTTT 475  
QY 121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140  
DB 476 GAAATTTATGATCCCATGATTTCTGTGCTTGAACACAGGCTACGCTATGCCAGGCTG 535  
QY 141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisIleLeuTyrPheTyrHisValGln 160  
DB 536 CTGACTTTTTCACGCTCATTTTGGCTATCTGATCATCTTAATTTTATCACGCTCAG 595  
QY 161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgValAlaLeuArg 180  
DB 596 TGTGCTGGAGTGAAGGTACAGAGTACCGCATGAGCCATGATTAATTTGGAAGGACCTTGT 655  
QY 181 LeuSerAsnMetAlaMetGlyIleThrThrGlyGlnIleValAsnLeuLeuSerAsn 200  
DB 656 CTTAGTATACATGCGCATGAGGAAAGACACACAGGCCGATATGCAATCTGCTGCAT 715  
QY 201 AspValAsnIlePheAspGlnValThrValPheLeuHisIlePheLeuTyrAlaGlyProLeu 220  
DB 716 GATGTGAACAAGTTTGAATCAGGTGACAGTGTCTTACACTTCTGTGGGACAGACACTG 775  
QY 221 GlnAlaIleAlaValThrAlaLeuLeuTyrMetGluIleGlyIleSerCysLeuAlaGly 240  
DB 776 CAGGAGATCGAGTACGACCTCTCTGATGAGATGAGAAATTCGTGCTTGTGAG 835  
QY 241 MetAlaValLeuIleIleLeuLeuProLeuInsSerCysPheGlyIleLeuPheSerSer 260  
DB 836 ATGGAGTCTTATCATTTCTCTGCTTGAAGCTTTTGGGAATTTGTTCTCATCA 895  
QY 261 LeuArgSerIleThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280  
DB 896 CTGAGGAGTAAACCTGCAATTTCAAGATCCAGATCAGAGCATGATGAATGAATGATTA 955  
QY 281 ThrGlyIleArgIleIleIleValMetCysTyrAlaTrpGluIleSerPheSerAsnLeuIleThr 300  
DB 956 ACTGTATTAAGATTAATTAATTAATGACCTGCGGAAAGTATTTCAATCTTATTAACC 1015  
QY 301 AsnLeuArgIleGlyGluIleSerIleIleLeuArgSerSerCysLeuArgIleMetAsn 320  
DB 1016 AATTTGAGAAAGAGAGATTTCCAGATTTCTGAGAGATTTCTGCTTACAGGAGATGAT 1075  
QY 321 LeuAlaSerPhePheSerAlaSerIleIleIleValPheValThrPheThrThrTyrVal 340  
DB 1076 TTGGCTTCTTTTTCAGTGAAGCAAAATCATCGTGTGAGACCTTCAACCACTTACGCTG 1135  
QY 341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyVal 360  
DB 1136 CTCTCTGCGAGTGTATCACAGCCGCGGTGTCTGCGAGTGAACCTGTATGAGGCT 1195  
QY 361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGlnAlaIle 380  
DB 1196 GTGCGGCTGACGTTTACCTTCTTCTTCCCTCAGAGCATGAGAGGTGTCAAGAGCAATC 1255  
QY 381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400  
DB 1256 GTCAAGATCCGAGAGATCCAGACCTTTTGTACTGTATGATATACACAGCAACCGCT 1315

QY 401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTyrAsp 420  
DB 1316 CAGTGGCCGTCAGATGGTAAAAAGATGGTCAGATGGATTTACTCTTTTGGGAT 1375  
QY 421 LysAlaSerGlnThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGlnLeu 440  
DB 1376 AAGGCATCGAAGACCCCACTACAGAGCCCTTCTTACGTCAGACCTGGCAATGG 1435  
QY 441 LeuAlaValAlaGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460  
DB 1436 TTAGCTGTGGTGGCCCTGGAGAGAGGAACTCATCTGTAAAGTCCCTGCTGGG 1495  
QY 461 GlnLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480  
DB 1496 GAATTGGCCCCAAGTCACGGGCTGGTCACGTCGACGAAGAATTGCTATGCTCTCAG 1555  
QY 481 GlnProTyrValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGln 500  
DB 1556 CAGCCCTGGGTGTCTCGGGAACTCGAGAGATTAATTTATTTGGGAAGAAATATGAA 1615  
QY 501 LysGlnArgTyrGlyLysValIleLysValaCysAlaLeuLysLysAspLeuGlnLeuLeu 520  
DB 1616 AAGGAAGCATATGAAGAAAGTCATTAAGCTTGTGCTGAAAAGATTTACAGCTGTG 1675  
QY 521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyLys 540  
DB 1676 GAGGATGTGATCTGATCTGATAGAGATCGGGAAACACGCTGAGTGAAGGCGAAGAA 1735  
QY 541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560  
DB 1736 GACGGGGTAAACCTTGCAAGAGCATGTATCAAGATCTGACATCTATCTCTGACAGAT 1795  
QY 561 ProLeuSerAlaValAspAlaGlnValSerArgHisLeuPheGlyLeuGlyLysCysGln 580  
DB 1796 CCTCTCAGTGCAGTATGCGAAGTTCAGACAGACACTTGTGCACTGTGATTTGTCTCA 1855  
QY 581 IleLeuHisGlyLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaAla 600  
DB 1856 ATTTTGCATGAGAAAGATCAAAATTTTATGATCATCATCACTGACAGTCAAAAGCTGCA 1915  
QY 601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGlnPhe 620  
DB 1916 AGTCAGATTCGATATTAAGATGGTAAATGGTGCAGAAAGGCGACTTACCTGATGTC 1975  
QY 621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGlnLysSerGlnGln 640  
DB 1976 CTAAATCTGATATGATTTTGGCTCCCTTTAAAGATGATATAGAGAAAGTGAACA 2035  
QY 641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGlnSerSerValTyr 660  
DB 2036 CCTCCAGTTCAGAGAACTCCCACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTGG 2095  
QY 661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGlnSerGlnAspThrGln 680  
DB 2096 TCTCAACAATCTTACAGCCCTCTTGAAGATGGTCTCTGAGAGCCAAAGATATAGAG 2155  
QY 681 AsnValProValThrLeuSerGlnGlnAsnArgSerGlyLysValGlyPheGlnAla 700  
DB 2156 AATGTCCTCAGTTCACATATCAGAGAGAAACCGTTCGAAGAAAGATTTGGTTTCAGGCC 2215  
QY 701 TyrLysAsnTyrPheArgAlaGlyAlaHisTyrPheIleValPheIlePheLeuIleLeuLeu 720  
DB 2216 TATTAAGAAATTAATCTCAGAGCTGGTGTCTCATGTGATTTCTTATTTCTCTTA 2275  
QY 721 AsnThrAlaAlaGlnAlaTyrValIleLeuGlnAspTyrTyrLeuSerTyrTyrAlaAsn 740  
DB 2276 AACACTGCAGCTCAAGGTGCTATATGCTTCAAGATGGTGGCTTTCATACATCGGGAAC 2335  
QY 741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyLysAsnValThrGlnLysLeuAsp 760  
DB 2336 AAAACAAGATATGCTAAATGCTCACTGATTAATGAGAGAGAAATTAACCAAGAAAGTACAT 2395  
QY 761 LeuAsnTyrTyrLeuGlyLysTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780

DB 2396 CTTAACTGTACTATAGAAATTTATTCAGGTTTAACTGATGACCTGTTCTTTGGCATTA 2455  
QY 761 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800  
DB 2456 GCAGATCTCTATTTGGTATTTCTACGTCCTTTTAACTTTCACAAACTTTCACACAGAA 2515  
QY 801 MetPheGlnSerIleLeuLysAlaProValLeuPheAspArgAsnProIleGlyArg 820  
DB 2516 ATGTTTGACAAATCTGAAGCTCCGGTATTAATTTATTTGATAGAAATCCAATAGGAAGA 2575  
QY 821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840  
DB 2576 ATTTTAAATCGTTTCTCCAAAGACATTCGACATTCGATGATTTGCTGCCCTGACGTTT 2635  
QY 841 LeuAspPheIleGlnThrLeuLeuGlnAlaValGlyValaSerValaValaValaVal 860  
DB 2636 TTAGATTTCAATCCAGACATTCGTACAGTGGTGGTGTGCTGTGCTGTGGCTGGCCCTG 2695  
QY 861 IleProTyrIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880  
DB 2696 ATTCCTTGATCGCAATACCTTGGTCCCTTGGAAATCATTTTCTTCTCGCGCA 2755  
QY 881 TyrPheLeuGlnThrSerArgAspValLysArgLeuGlnSerThrThrArgSerProVal 900  
DB 2756 TATTTTGGAAACGTCAAGAGATGTGAAGCGCTGGATCTACACATCGGAGTCCAGTG 2815  
QY 901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTyrThrIleArgAlaTyrLysAlaGln 920  
DB 2816 TTTTCCACTGTGTATCTTCTCTCCAGGGGCTGTGACATCCGGGACATCAAGAGCAAGAA 2875  
QY 921 GluArgCysGlnGlnLeuPheAspAlaHisGlnAspLeuHisSerGlnAlaIleTyrPheLeu 940  
DB 2876 GAGAGGTCTCAGAACTGTTGATGCACACAGATTTTACATTCAGAGGCTTGGTCTTGG 2935  
QY 941 PheLeuThrThrSerArgTyrPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960  
DB 2936 TTTTGGACAAAGCTCCCGGTGGTGGCGCTGCTGATGACATCTGTGCCATGTTGTTC 2995  
QY 961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyIleValGly 980  
DB 2996 ATCATCTGTGCTTTGGTCCCTGATCTTGCCAAAGAACTCGAGATCCGGGACAGTTGGT 3055  
QY 981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTyrCysValArgGlnSer 1000  
DB 3056 TTGGCAGTCTCTAATGCCCTCACGCTCATGGGAGATGTTTCACTGAGTGTGTCACAAAGT 3115  
QY 1001 AlaGlyValGlnAsnMetMetIleSerValGlnArgValIleGlnTyrThrAspLeuGln 1020  
DB 3116 GCTGAAGTTGAGAAATATGATATCTCAGTAAAGAGGTCAATTAATACAGACACTTGA 3175  
QY 1021 LysGlnAlaProTyrGlnTyrGlnLysArgProProAlaTyrProHisGlyGlyVal 1040  
DB 3176 AAGAGACACTTGGGAATATCAAGAAAGCCACACACAGCTGGCCCAAGAGAGATG 3235  
QY 1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060  
DB 3236 ATTAATCTTGAACAATGTAATCTCATGTACAGTCCAGGTGGGCTCTGTACTGAAGCAT 3295  
QY 1061 LeuThrAlaLeuIleLysSerGlnGlnLysValGlyIleValGlyArgThrGlyValaGly 1080  
DB 3296 CTGACAGACACTTAATTAATCAACAGAAAGGTGGCATTTGGGAAGAACCGGAGCTGGA 3355  
QY 1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGlnProGlnGlyLysIleTyrPhe 1100  
DB 3356 AAAAGTCCCTCATCTACGCCCTTTTATGATTTGTCAAGACCGAAGATTAATTTGGATT 3415  
QY 1101 AspLysIleLeuThrThrGlnIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120  
DB 3416 GATAAGATCTTGAACAATGGAATTCGATTCACGATTTAAGAGAAATATGATCATCATTA 3475  
QY 1121 ProGlnGlnProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGln 1140



Db 3476 CCTCAGAACCTGTTTGTTCATCGGAACATGAGGAAAACTGTGATCCCTTTAAGANG 3535  
Qy 1141 HserrapagluuLeuThraapalaleuugluValGluLeuValGluThrlleGlu 1160  
Db 3536 CACAGAGATGAGAACTGTGATGATCCTTACAGAGGTACCACTTAAGAAACCAATTGA 3595  
Qy 1161 AspleuproglyLyseMetAspThrGluLeuValagluSerGlySerAspPheSerValGly 1180  
Db 3596 GATCTTCCTCGTAAATGATCTGTAATTAAGAGATCAGATCCAAATTTTAGTGTGA 3655  
Qy 1181 GluValGluLeuValCysLeuValaargalaleuValgylValGluGluLeuLeu 1200  
Db 3656 CAAGAACCACTGTGTGCTTGTCCAGGCGCAATTCAGGAAAAATCAGATATTGATTAT 3715  
Qy 1201 AspgluValaThraAlaasnValaspProargThraapgluLeuileGluValyllearg 1220  
Db 3716 GATGAAGGACGCGCAATGTGATCCAGAACTGATGATTATACAAAAAAATCCGG 3775  
Qy 1221 GluValPheAlaHisCysThrValLeuThrlleAlaHisargLeuAsnThrlleAsp 1240  
Db 3776 GAGAAATTTGCCCACTGCACCTGTCTAACATTGCACACAGTTGAACACCTTTTAC 3835  
Qy 1241 SerAspValleMetValleuaspSerGlyargLeuValgyluTyraapgluProTyraVal 1260  
Db 3836 AGCGACAGATPATGTGTTTATGATTCAGGAAGACTGAAAGAAATATGATGAGCCGTATGT 3895  
Qy 1261 LeuLeuGluAsnValGluSerleuPheThryllyseMetValGluGluLeuValaglu 1280  
Db 3896 TTGCTGCAAAATTAAGAGAGCTTATTTTACAGAGGTGCAACACTGGCAGAGCAAA 3955  
Qy 1281 AlaAlaAlaLeuThrlleGluThraAlaValgyluValTyraPheValArgAsnTyraProHisle 1300  
Db 3956 GCCGTGCTTCCTCAGCAAGAACGCAAAACAGGTATCTTCMAAGAAATTTATCCATAT 4015  
Qy 1301 GlyHisThrAspHisMetValThrAsnThraSerAsnGlyGluProSerThrlleThrlle 1320  
Db 4016 GGTCACTGACCAATGATGTTTACAAACACTTCATATGACAGCCCTGCACCTTACTAT 4075  
Qy 1321 PheGluThraAlaLeu 1325  
Db 4076 TTCGAGACGACCTG 4090

RESULT 12  
ACLS8944  
ID ACLS8944 standard: CDNA: 4231 BP.  
XX ACLS8944;  
AC 24-MAR-2005 (first entry)  
DT 24-MAR-2005 (first entry)  
XX  
DE ABCC4 coding sequence, SEQ ID 1.  
XX  
KW Cytostatic; Gene therapy; Vaccine; RNA interference; cancer; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO2005001092-A2.  
XX  
PD 06-JAN-2005.  
XX  
PF 19-MAY-2004; 2004MO-US015645.  
XX  
PR 20-MAY-2003; 2003US-0471729P.  
XX  
PA (AMHP) WYETH.  
XX  
PI Be X, Wei L, Slonim DK, Howes SH;  
XX  
DR WPI, 2005-075568/08.  
XX  
DR P-FSDB; ABR93962.  
XX  
PT Pharmaceutical composition comprising an agent modulating an  
expression level or protein activity of a gene, e.g. ABCC4, or a T cell

PT activated by the polypeptide or antibody, and a carrier, useful for  
PT treating cancer.  
PS Claim 8; SEQ ID NO 1; 113pp; English.  
XX  
CC The present invention relates to a novel pharmaceutical composition  
CC comprising: (a) an agent capable of modulating an expression level or  
CC protein activity of a cancer-related transmembrane protein (CRTP) or gene  
CC ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and  
CC (b) a carrier. The pharmaceutical composition may also comprise a  
CC polynucleotide capable of inhibiting or decreasing the expression of the  
CC CRTP by RNA interference or an antisense mechanism. The CRTPs of the  
CC invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,  
CC FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The  
CC pharmaceutical composition is useful for treating cancer, e.g. colon  
CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney  
CC cancer, stomach cancer, and esophageal cancer. The present sequence is  
CC the coding sequence for one such CRTP. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX  
SQ Sequence 4231 BP; 1170 A; 895 C; 1015 G; 1151 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 0 Length: 4231  
Score: 6779.00 Matches: 1323  
Percent Similarity: 99.9% Conservative: 1  
Best Local Similarity: 99.8% Mismatches: 1  
Query Match: 99.9% Indels: 0  
DB: 14 Gaps: 0

US-09-976-858-42 (1-1325) x ACLS8944 (1-4231)  
Qy 1 MetLeuProValTyrgluValValleProAsnProleuGluInaapAlaasnLeuCysSer 20  
Db 116 ATGTCGCCCGGTACAGAGAGGTGAAGCCCAACCGCTGCAGAGCGCAACATCGTCA 175  
Qy 21 ArgValPhePheTrpTyrPleuAsnProleuPheValleGlyHisValArgArgLeuGlu 40  
Db 176 CGCGTGTCTTCGTGCTCAATCCCTGTTTAAATGGCCATTAACGAGATTGAG 235  
Qy 41 GluAspAspMetTyraSerValleuProGluAspArgSerGluHisleuGlyGluLeu 60  
Db 236 GAAGATGATATGATTTACGCTCTCCAGAGACCGCTCAGACGACTTGGAGAGAGTTG 295  
Qy 61 GluGlyPheTrpAspValgyluValleuArgAlaGluAsnAspAlaGluValProSerleu 80  
Db 296 CAAGGTTCTCGATTAAGAAAGTTTAAAGCTGAGATGACGACAGAACCTTCTTTA 355  
Qy 81 ThrArgAlaIlelleValCysTyrrTyrPleuSerTyraValleuGlyllePheThrlleu 100  
Db 356 ACAAGAGCAATCAATTAAGTGTACTGAAATCTTATTTAGTTTGGAAATTTTAACTGA 415  
Qy 101 IleGluGluSerAlaValleuIleGluProIlePheleuGlyValleAsnTyraPhe 120  
Db 416 ATTGAAGAAAGTCCAAAGTATATCAGCCCATTTTGGAAATTTTAAATTTATTTT 475  
Qy 121 GluAsnTyraapPrometAspSerValAlaLeuAsnThraAlaTyraAlaThraVal 140  
Db 476 GAAATTTATGATCCCATGAGATTCGTGGCTTTGAACACAGGTACGCTATGACAGGTG 535  
Qy 141 LeuThrPheCysThrLeuIleleuAlaIleleuHisleuTyrrPheTyrrHisValGlu 160  
Db 536 CTGACTTTTGCAGCGCTATTTGGCTATATCTGATCATCTATATTTTATCAGGTTGAG 595  
Qy 161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyraGlyValAlaLeuArg 180  
Db 596 TGTCTGGATGAGGTTTACAGTACAGTACGATGTCATATGATTTATCGAAGGCACTTCGT 655  
Qy 181 LeuSerAsnMetAlaMetGlyTyrrThrlleGluGluValleuLeuLeuSerAsn 200  
Db 656 CTTAGTAAATGCGCATGCGGGAAGACCAACCAAGCCAGATGATGCAATCTGCTCCAAAT 715

QY 201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220  
 Db 716 GATGTGAACAAAGTTTGATCAGAGTGACAGTGTCTTACACTTCCTGTGGCAGACCACTG 775  
 QY 221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGlnIleGlyTyrIleSerGlyLeuAlaGly 240  
 Db 776 CAGGGGATCGCAGATGCTGCCCTACTCTGGATGGATGGAAATTCGGTCCCTTCTGGG 835  
 QY 241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260  
 Db 836 ATGGCAATCTTAATCAATCTTCTGCTGCCCTTGCAGAAAGCTGTGTTGGAAAGTTGTTCACTA 895  
 QY 261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280  
 Db 896 CTGAGAGTAATAAATCGCAACTTTCACGAGATGCAGAGATCAGAGCAATGAATGAAGTTATA 955  
 QY 281 ThrGlyTyrArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300  
 Db 956 ACTGGTATAGATATATAATAAATGTACGCTGGGAAAGTCAATTTTCATATCTTATTTACC 1015  
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 Db 1016 AATTTGAGAAAGAGAGATTTCCAGATTTCTGAGAAAGTTCTGCTTCAGGGGATGAAT 1075  
 QY 321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340  
 Db 1076 TTGGCTTCGTTTTTTCAGTCAAGCAAAATCATCGTGTGTCGACCTTCAACCACTTACGCTG 1135  
 QY 341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyVala 360  
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 QY 421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440  
 Db 1376 AAGGATCGAGAACCCCACTTACAGAGCCTTTTCTTACTGTCTGACTGCGCAATTG 1435  
 QY 441 LeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460  
 Db 1436 TTAGCTGTGTGCGCCCGTGGGAGCAGGAAGTATCATCTGTAAAGTCCCGTCCGCG 1495  
 QY 461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaIleValSerGln 480  
 Db 1496 GAATTGTGCCCAAGTCAACGGCTGTGTCAACGCTGCAGGAAGAAATGCCATATGTCTCG 1555  
 QY 481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGln 500  
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 QY 501 LysGluArgTyrGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520  
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 QY 521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540  
 Db 1676 GAGGATGGTATCTGATGTATGAGATCGGGGAACCAACGCTGTGTGAGAGGCGCAAAA 1735  
 QY 541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560  
 Db 1736 GACGGGTTAACTTTCAGAGAGCAAGTGTATCAAGATGCTGACATCTATCTCTGAGCAAT 1795

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 QY 641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGlnSerSerValTrp 660  
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Db      2876 GAGAGGTGCAGGAACTGTTTATGACACCGAGATTTCATTGAGAGCTTGTTCTTG 2935
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Db      2936 TTTTGGACACACGTCCTGGTGTGCGCCGTCCTGGATGATCCATGTCCTCATGTTTGTTC 2995
Qy      961 IleIleValAlaPheGlySerLeuIleLeuAlaIleValThrLeuAspAlaGlyValGly 980
Db      2996 ATCATGCTTGCTTGGGTCCTTGATCTGGCAAAACTGGATGCCGGGAGGTTGGT 3055
Qy      981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgGlnSer 1000
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Qy      1001 AlaGlyValGlyAsnMetCylSerValGlyArgValIleGlyTrpThrAspLeuGly 1020
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Qy      1101 AspLysIleLeuThrThrGlyIleGlyLeuHisAspLeuArgLysMetSerIleIle 1120
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Qy      1201 AspGlyAlaThrAlaAsnValAsnProArgTrpAspGlyLeuIleGlnLysLysIleArg 1220
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Qy      1221 GlyLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240
Db      3776 GAGAAATTTGCCCATCGCACCTGCTACCATTTGACACAGATGGAACCATTTATTGAC 3835
Qy      1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGlyTrpAspGlyProTyrVal 1260
Db      3836 AGCGCAAGATATATGTTTATGATTCAGAGACACTGAAGAAATATGATAGCGGTATGTT 3895
Qy      1261 LeuLeuGlnAsnLysGlySerLeuPheTyrLysMetValGlyGlnLeuGlyLysAlaGly 1280
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Qy      1281 AlaAlaAlaLeuThrGlyThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300

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Db      3956 GCCGCTGCCCTCACTGAAGACAGAAACAGGTACTTCAAAAGAAATATTCACATATT 4015
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Db      4016 GGTCACTGACCAACATGTTTAAACAACTTCATGACAGAGCCCTGACCTTAACATT 4075
Qy      1321 PheGlyThrAlaLeu 1325
Db      4076 TTCAGACAGCACTG 4090

RESULT 13
AEA00097
ID AEA00097 standard; cDNA, 4231 BP.
XX
AC AEA00097;
XX
DT 28-JUL-2005 (first entry)
XX
DE Human TAT131 cDNA SEQ ID NO:49.
XX
KW ss; gene; tumor-associated antigen; cytostatic; breast tumor;
KW endocrine disease; gynecology and obstetrics; neoplasm; colon tumor;
KW gastrointestinal disease; rectal tumor; endometroid carcinoma;
KW genitourinary disease; renal tumor; lung tumor; respiratory disease;
KW ovary tumor; skin tumor; liver tumor.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
FT CDS 116..4093
FT /tag= a
FT /product= "TAT131"
XX
PN US2005106644-A1.
XX
PD 19-MAY-2005.
XX
PP 08-SEP-2004; 2004US-00936626.
XX
PR 20-JUN-2001; 2001US-0299500P.
PR 29-JUN-2001; 2001US-030180P.
PR 18-SEP-2001; 2001US-0323268P.
PR 19-JUN-2002; 2002US-0017748P.
PR 26-MAR-2004; 2004US-0557115P.
PR 04-AUG-2004; 2004US-0596899P.
XX
PA (GENTH ) GENTECH INC.
XX
PI Cairns B, Chen R, Frantz G, Hillan KJ, Koepfen H, Phillips HS;
PI Polakie P, Spencer SD, Smith V, Williams PM, Wu TD, Zhang Z;
PI Sliwkowski M;
XX
DR WPI, 2005-384304/39.
DR P-PSDB; AEA00175.
XX
PT Novel isolated antibody capable of binding to tumor-associated antigenic
PT target polypeptide, useful for treating cell proliferative disorder e.g.
PT cancer.
XX
PS Claim 1; SEQ ID NO 49; 337pp; English.
XX
CC The invention relates to a novel isolated antibody binding to a
CC polypeptide having at least 80% sequence identity to a polypeptide having
CC any one of 76 fully defined 182-910 amino acid tumor-associated antigenic
CC target polypeptide (TAT) sequences (AEA00127-AEA00202) given in the
CC specification, a polypeptide having any one of (AEA00127-AEA00202),
CC lacking its associated signal peptide, or an extracellular domain of a
CC polypeptide having any one of (AEA00127-AEA00202). The polypeptide is
CC encoded by the nucleotide sequence having any one of (AEA00049-AEA00126).
CC An antibody of the invention has cytostatic activity. The antibody is
CC useful for inhibiting growth of a cell expressing TAT188, which involves
CC contacting the cell with the antibody. The cell is a cancer cell chosen
CC from breast, colon, rectum, endometrium, kidney, lung, ovary, skin and

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CC liver cell. The cancer cell is a mammalian cell, preferably a human cell.  
 CC The antibody is also useful for detecting the level of TAT188  
 CC polypeptide expressed in a test cell relative to a control cell, and for  
 CC detecting the level of TAT188 polypeptide or a polypeptide having at  
 CC least 80 % sequence identity to the TAT188 polypeptide sequence in a test  
 CC cell relative to a control cell. The antibody is useful for treating a  
 CC preventing a cell proliferative disorder associated with increased  
 CC expression or activity of a polypeptide having at least 80 % identity to  
 CC a TAT188 polypeptide sequence. The cell proliferative disorder is cancer.  
 CC The method of the invention is useful for inhibiting the growth of a  
 CC cancer cell. The present sequence encodes a polypeptide of the invention.

XX Sequence 4231 BP, 1170 A, 895 C, 1015 G, 1151 T, 0 U, 0 Other;

## Alignment Scores:

Pred. No.:	0	Length:	4231
Score:	6779.00	Matches:	1323
Percent Similarity:	99.9%	Conservative:	1
Best Local Similarity:	99.8%	Mismatches:	1
Query Match:	99.9%	Indels:	0
DB:	14	Gaps:	0

US-09-976-858-42 (1-1325) x AEA00097 (1-4231)

QY 1 MetLeuProValTyrGlnValValProAsnProLeuGlnAspAlaAsnLeuCySer 20  
 DB 116 ATGCTCCCGTGTACAGAGAGGTGAAGCCCAACCCGCTGAGGACGCAATCTGCTCA 175  
 QY 21 ArgValPhePheTrpTrpLeuAsnProLeuPheValIleGlyHisValArgTrpGlu 40  
 DB 176 CCGGTGTTCTTCTGGTGTCAATCCCTGTTTAAATGGCCATTAACGGAGATTAGAG 235  
 QY 41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGlnLeu 60  
 DB 236 GAAAGATGATGATGATTCAGTGTCCGCAAGACCGCTCAACGACCTTGGAAGAGATTG 295  
 QY 61 GlnGlyPheTrpAspTrpGlyValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80  
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 QY 81 ThrArgAlaIleIleIleValCysTrpTyrTrpLysSerTyrLeuValLeuGlyLepheThrLeu 100  
 DB 356 ACAAGACATCATTAAGTGTATCTGAAATCTTATTAGTTTGGAAATTTTTCGTGA 415  
 QY 101 IleGlnGluSerAlaValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120  
 DB 416 ATTGAGGAAGTCCCAAGTATCCAGCCCATTTTGGGAAAATTTTAAATTATTTT 475  
 QY 121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaThrVal 140  
 DB 476 GAAATTTATGATCCCATGATTTCTGTGCTTGACACAGCGTACCGCTATGCCAGG 535  
 QY 141 LeuThrPheCysThrIleuIleuAlaIleuHisIleuTyrPheTyrHisValGln 160  
 DB 536 CTGACTTTTGGACCGTCAATTTGGCTATATCTGCACACTTAAATTTTATACGTTG 595  
 QY 161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180  
 DB 596 TGTGCTGGATGAGGTTCAGAGTACGATGCTGCAATGATTTATGGAAGCACTTCGT 655  
 QY 181 LeuSerAsnMetAlaMetGlyLysTrpThrTrpGlnIleValAsnLeuLeuSerAsn 200  
 DB 656 CTTAGTAACATGGCCATGGGAAAGACACACAGGCGCAGATAGTCAATCTGCTGCAT 715  
 QY 201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220  
 DB 716 GATGTGAACAAGTTTATCATGAGTGACAGAGTCTTACCTCTGTGGCAGACACACTG 775  
 QY 221 GlnAlaIleAlaValThrAlaLeuLeuTyrMetGlnIleGlyLysSerCysLeuAlaGly 240  
 DB 776 CAGGCATGCACTGATGCTGCTGATGAGATGAAATATGATCGCTTGTCTGGG 835  
 QY 241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260

DB 836 ATGGAGTTCATATCATCTCTGCTGCAAGGCTGTTTGGAACTTGTTCATCA 895  
 QY 261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgTrpMetAsnGlyValIle 280  
 DB 896 CTGAGAGTAAACTGCACATCTTACGAGATCCAGATCCAGACCATTAAGAACTTATA 955  
 QY 281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGlyLysSerPheSerAsnLeuIleThr 300  
 DB 956 ACTGGTATTAAGATATTAATAATGACCGCTGGGAAAGTATTTTCAAACTTATATACC 1015  
 QY 301 AsnLeuAlaGlyLysGlnIleSerTyrIleLeuArgSerSerCysLeuArgGlyMetAsn 320  
 DB 1016 AATTGAGAAAGAAAGAAATTTCCAAAGATTCGAGAAATTCCTGCTTACGAGGATGAT 1075  
 QY 321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrTyrVal 340  
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 DB 1376 AAGGATCAGAGACCCCAACTCTACMAAGCCCTTCTTCTGTCAGCCGTGGCAATTG 1435  
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Db 2816 TTTTCCCACTTGTCAATCTTCTCTCCAGGGGCTCTGGACATCCGGGCAACAAAGAGAGA 2875  
Qy 921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGlnAlaTrpPheLeu 940  
Db 2876 GAGAGGTGTCAAGAACTGTTTATGACACACAGGATTTACATTCAGAGGCTTGGTCTTG 2935  
Qy 941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960  
Db 2936 TTTTGGACAAAGCTCCGCTGGTTCGCGCTCCGCTGGATGCCATTCGTCCACAGTTTGTG 2995  
Qy 961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980  
Db 2996 ATCATGCTGTGCTTGGGTCCCTGATTCGGCAAAAACCTGGATGCCGGGCAAGTTGGT 3055

Qy 981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTyrCysValArgGlnSer 1000  
Db 3056 TTGGCACTGTCTTATGCTTCACTGCTCATGGGGAATGTTTCAGTGGTGTGACAAAGT 3115  
Qy 1001 AlaGlnValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGln 1020  
Db 3116 GCTGAAGTTGGAATATATATATATCTCACTAAGAAAGGCTCATTTGAATACAGACCTTGA 3175  
Qy 1021 LysGlnAlaProTyrGluTyrGlnLysArgProProAlaTyrProHisGluGlyVal 1040  
Db 3176 AAAGAAGCACTTGGGAATATCAGAAACCCACCAACAGCTGGCCCCCATAGAGAGAGT 3235  
Qy 1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060  
Db 3236 ATTAATCTTGAACAAATGTAATCTCAATGACAGTCCAGAGTGGGCTCTGGTACTGAAGCAT 3295  
Qy 1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080  
Db 3296 CTGACAGCATCTATTAATTCACAAAGAAAGTGGCATTTGGGAAGAAACCGAGCTGGA 3355  
Qy 1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100  
Db 3356 AAAAGTCCCTCATCTCAGCCCTTTTATGATGTGCAGAAACCGAAGTAAATTTGGATT 3415  
Qy 1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuAspGlyLysMetSerIleIle 1120  
Db 3416 GATAAGATCTTGACAACTGAATTTGAGCTTCAACGATTTAAGAAAGAAATGTCATTCATA 3475  
Qy 1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140  
Db 3476 CCTCAGGAACCTGTTTGTTCACCTGACCTGAACATAGGAAGAAACCTGGATCCCTTAAAGAG 3535  
Qy 1141 HisThrAspGluGluLeuTyrAsnAlaLeuGlnGlnValGlnLeuLysGluThrIleGlu 1160  
Db 3536 CACAGGATGAGAACTGTGGAATGCTTACCAAGAGGTACAACTTAAAGAAACCACTTGA 3595  
Qy 1161 AspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180  
Db 3596 GATCTTCTGTGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 3655  
Qy 1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200  
Db 3656 CAAGACAACTGTGTGCTTGCCTTGCAGGGCAATTCACAGAAAAACAGATATTTGATT 3715  
Qy 1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220  
Db 3716 GATGAAGGACGGCAAAATGTGATCCAAAGACTGATGATTAAATCAAAAAAAATCCGG 3775  
Qy 1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleLeuP 1240  
Db 3776 GAGAAATTTGGCCCATGACCGGTGTAACTTGTACACAGATTTAACAACCATTTTGAAC 3835  
Qy 1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGlyLysTyrAspGluProTyrVal 1260  
Db 3836 AGCGCAAGATATATGTTTATGATTACAGAAAGCTGAAGAAATATGATGAGCCGATGTT 3895  
Qy 1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGln 1280  
Db 3896 TTGCTGCAAAATTAAGAGAGCTTATTTACAAAGATGTGCAACCACTGGGCAAGCAADA 3955  
Qy 1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300  
Db 3956 GCCGTGCCCTTCACTGAAGACGAAACAGGATATCTTCAAAAGAAATATTCACATATTT 4015  
Qy 1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320  
Db 4016 GGTCACTGACCAATGATTTACAAACACTTCATATGACAGCCCTCACTTAATCTATT 4075  
Qy 1321 PheGluThrAlaLeu 1325  
Db 4076 TTGAGAGACAGCACTG 4090

RESULT 14  
 ID AEA00617  
 AEA00617 standard; cDNA; 4231 BP.  
 AC AEA00617;  
 DT 28-JUL-2005 (first entry)  
 DE Human TAT131 cDNA sequence SeqID49.  
 KM antibody identification; tumor-associated antigen; cytostatic;  
 KM RNA interference; gene therapy; cell death; cancer; breast tumor;  
 KM colon tumor; rectal tumor; renal tumor; lung tumor; ovary tumor;  
 KM skin tumor; liver tumor; gene; ss; TAT131.  
 OS Homo sapiens.  
 PN US2005107595-A1.  
 PD 19-MAY-2005.  
 PF 10-SEP-2004; 2004US-00938061.  
 XX 20-JUN-2001; 2001US-0299500P.  
 XX 29-JUN-2001; 2001US-0301880P.  
 XX 18-SEP-2001; 2001US-0323268P.  
 XX 19-JUN-2002; 2002US-00177488.  
 XX 26-MAR-2004; 2004US-0557116P.  
 XX 04-AUG-2004; 2004US-0598899P.  
 XX (GENTH ) GENENTECH INC.  
 XX Cairns B, Chen R, Frantz G, Hillan KJ, Koepfen H, Phillips HS;  
 PI Polakis P, Spencer SD, Smith V, Williams PM, Wu TD, Zhang Z;  
 PI Sakanaka C, Chundharapai A, Reed CJ;  
 DR WPI; 2005-371577/38.  
 DR P-PSDB; AEA00695.  
 XX  
 PT Novel isolated antibody e.g. anti-R16 or anti-TAT112 antibody that binds  
 PT to tumor-associated antigenic target polypeptide, useful for diagnosing  
 PT or treating cancer.  
 XX  
 XX Claim 1; SEQ ID NO 49; 96pp; English.  
 XX  
 CC This invention relates to a novel isolated antibody, for example anti-R16  
 CC or anti-TAT112 antibody, that binds to a tumor-associated antigenic  
 CC target polypeptide (TAT) and that lacks an associated signal peptide  
 CC sequence. The invention may be useful for the development of compounds  
 CC with a cytostatic activity acting as antagonists of the TAT118  
 CC polypeptide or RNA interference whilst the disclosed sequences may be  
 CC useful for gene therapy. The invention is useful for inducing the death  
 CC of a cell (such as a cancer cell chosen from breast, colon, rectum,  
 CC endometrium, kidney, lung, ovary, skin and liver) to which it binds,  
 CC inhibiting proliferation or promoting cell death of a cell expressing  
 CC TAT118. In addition, the invention may be useful for detecting the level  
 CC of TAT118 polypeptide in a test cell relative to a control cell, or  
 CC treating or preventing a cell proliferative disorder associated with  
 CC increased expression of TAT118. The novel antibody of the invention is  
 CC useful for inhibiting the growth of a cancer cell and may be useful for  
 CC diagnosing or treating cancer. The present sequence is that of the human  
 CC TAT131 cDNA which encodes a protein against which an antibody of the  
 CC invention may be targeted.  
 XX  
 SO Sequence 4231 BP; 1170 A; 895 C; 1015 G; 1151 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 0  
 Score: 6779.00  
 Percent Similarity: 99.98  
 Best Local Similarity: 99.98  
 Query Match: 99.98  
 DB: 14

Length: 4231  
 Matches: 1323  
 Conservative: 1  
 Mismatches: 1  
 Indels: 0  
 Gaps: 0

US-09-976-858-42 (1-1325) x AEA00617 (1-4231)  
 QY 1 MetLeuProValTYrGlnGluValIlysrProAsnProLeuGlnAspAlAsnLeuCySer 20  
 Db 116 ATGCTGCCGCTGACAGAGGTGAAGCCCAACCCCTGCAGACGCACAACTGCTCA 175  
 QY 21 ArgValPhePheTrpTrpLeuAsnProLeuPheYsIIegYhIlyArGArgLeuGlu 40  
 Db 176 CGCGTGTTCTTGCTGCTCAATCCCTGTTTAAATTTGGCCATTAACGAGATTAGAG 235  
 QY 41 GluAspAspMetYrSerValLeuProGluAspArgSerGlnHsleuGlyGlnGluLeu 60  
 Db 236 GAAAGATGATATGATATTCAGTGTCCAGAAAGCCCTCAGACGACCTTGAGAGAGTTG 295  
 QY 61 GlnGlyPheTrpAspIlyGluValLeuArgAlaGluAspAlaGlnIlyProSerLeu 80  
 Db 296 CAAGGCTTCTGGATTAAGAAAGTTTAAAGCTGAATGACGACACAAAGCTTCTTA 355  
 QY 81 ThrArgAlaIleIleIlyeCyseYrTrpIlySerYrIleuValLeuGlyIlePheThrLeu 100  
 Db 356 ACAAGAGCAATCATTAAGTTACTGAAATCTTATTAGTTTGGAAATTTTACGTTA 415  
 QY 101 IleGlnIlySerAlaIlyeValIleGlnProIlePheLeuGlyIlyeIleAsnYrPhe 120  
 Db 416 ATTGAGAAAGTGCACAAAGTATCCAGCCCATATTTTGGAAAAATTATTAATTATTT 475  
 QY 121 GluAsnYrAspProMetAspSerValAlaLeuAsnThrAlaYrAlaYrAlaThrVal 140  
 Db 476 GAAATTTATGATCCCATGATTTCTGTGCTTGAACACAGCTACGCTATGCCAGGTG 535 -  
 QY 141 LeuThrPheCystrLeuIleleuAlaIleleuHsIshIleuYrPheYrHisValGln 160  
 Db 536 CTGACTTTTGGACCGCTATTTGGCTATACGATCACTTAATTTTATTCACGTTGAG 595  
 QY 161 CysAlaGlyMetArgLeuArgValAlaMetCysHsIsmetIleYrArgIlyAlaLeuArg 180  
 Db 596 TGTGCTGGATGAGGTTCAGAGTACGATGCGCATGATGATTTATCGAAGGACCTTGT 655  
 QY 181 LeuSerAsnMetAlaMetGlyIlyeThrThrThrGlyGlnIleValAsnLeuSerAsn 200  
 Db 656 CTTATGATACATGCGCATGGAGNAGCAACACAGGCCAGATGATCATCTGTGTCAT 715  
 QY 201 AspValaAsnIlyPheAspGlnValThrValPheleuHsIshleuLeuTrpAlaGlyProLeu 220  
 Db 716 GATGTGAACAAGTTTGATGACAGGTGACAGGTCTTACACTTCTGTGGGACGACACTG 775  
 QY 221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysleuAlaGly 240  
 Db 776 CAGGGGATCGCAGTACCTGCTTCTGATGAGATGAGAAATCGTGTCTGTGG 835  
 QY 241 MetAlaValleuIleIleleuLeuProLeuGlnSerCysPheGlyIlyeLeuPheSerSer 260  
 Db 836 ATGGCACTTCTAATCATTTCTCTGCTTGCACAACTGTTTGGAAAGTTGTTCACTCA 895  
 QY 261 LeuArgSerIlyeThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280  
 Db 896 CTGAGAGATTAAGTAACTGCAACTTTCACGATGCGACGATCAGACCATGATTAATTA 955  
 QY 281 ThrGlyIleArgIleIleIlyeMetYrAlaTrpGluIlySerPheSerAsnLeuIleThr 300  
 Db 956 ACTGATTAAGATTAATAAATGATGACCTGCGGAAAGTCATTTTCAATTTATTTACC 1015  
 QY 301 AsnLeuArgIlyeGluIleSerIlyeIleuArgSerSerCysLeuArgIlyeMetAsn 320  
 Db 1016 AATTGAGAAAGAAAGAGATTTTCAAGATTTCTGAGAAAGTTCTGCTCAGGGGAGTAA 1075  
 QY 321 LeuAlaSerPhePheSerAlaSerIlyeIleValIlePheValThrPheThrThrYrVal 340  
 Db 1076 TTGGCTTGCTTTTTCAGTGCAGCAAAATCATCGTGTGTTGACCTTCACCACTACGG 1135  
 QY 341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuYrGlyVala 360

Db 1136 CTCCTCGAGTGTGATCAGACCGCGTGTCTGTCAGTGCCTGATGAGGCGCT 1195  
 QY 361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380  
 Db 1196 GTGGCGCTGACGGTTACCTCTCTTCCCTCAAGCCATTGAGAGGGGTGCAGAGCGCAATC 1255  
 QY 381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArg 400  
 Db 1256 GTCAAGATCCGAAGATCCAGACCTTTTGTACTGATGAGATATCAAGCGCAACCGT 1315  
 QY 401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTyrPasp 420  
 Db 1316 CAGCTGCCCTCAGATGCTAAAGATGCTGACATGTGCAGATTTTACTCTTTTGGGAGT 1375  
 QY 421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440  
 Db 1376 AAGGACATCAGAGACCCCACTTACAGAGCCCTTTCTTTACGTGACAGCTGCGCAATGG 1435  
 QY 441 LeuAlaValAlaGlyProValGlyAlaGlyLysSerSerLeuSerAlaValLeuGly 460  
 Db 1436 TTAGCTGTGTGCGCCCTGGAGAGCGGAAGTCACTCTTAAAGTCCGTGCTCGGG 1495  
 QY 461 GlnLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480  
 Db 1496 GAATTGGCCCCAAGTCACGGGCTGGTCAAGCTGATGAGAAAGATTGCCATGTGCTCAG 1555  
 QY 481 GlnProTyrValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500  
 Db 1556 CAGCCCTGGTGTCTCTCGGGAACCTGAGAGAGTAATTTTATTTGGGAGAAATATGAA 1615  
 QY 501 LysGluArgTyrGlyLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520  
 Db 1616 AAGGACCATATGAAAAAGTCAATAAGCTTGTGCTCTGAAAAAGATTACAGCTGTGG 1675  
 QY 521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540  
 Db 1676 GAGGATGTGGATCTGACTGTGATAGGAGATCGGGGAAACACCGCTGAGTGAAGGCGAAA 1735  
 QY 541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspArg 560  
 Db 1736 GCAGCGGTAAACCTTGCAAGACAGTGTCAAGATGTCAGACATCTATCTCTGAGCGAT 1795  
 QY 561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGlyLeuLysGln 580  
 Db 1796 CCTCTCAGTGCAGTACGCGAAGTTCAGACACACTTTTCGAAGTGTGATTTTGTCAA 1855  
 QY 581 IleLeuHisGlyLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaIle 600  
 Db 1856 ATTTTGATGAGAGATGACAAATTTTATGATCACTCATCAGTTGCAGTACCTCAAGCTGCA 1915  
 QY 601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPhe 620  
 Db 1916 ACTCAGATTCTGATATGTGAAGATGTGTAATGTGTGCAGAGGGGCTTACACTGAGTTC 1975  
 QY 621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluLeuSerGluGln 640  
 Db 1976 CTTAAATCTGGATATGATTTTGGCTCCCTTTTAAAGAGATTAAGAGAAAGTGAACA 2035  
 QY 641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGlnSerSerValTyr 660  
 Db 2036 CCTCCAGTTCCAGGAACCTCCACACTAAGGAATCGTACTTCAGAGTCTTCGGTTGG 2095  
 QY 661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGlnSerGlnAspThrGlu 680  
 Db 2096 TCTCAACATCTTCTAGACCTCTCTTGAAGATGTGCTCTGAGAGCCCAACATACAGAG 2155  
 QY 681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAla 700  
 Db 2156 AATGTCCTCCAGTACACTATCAAGAGAACCGTTCTGAAAGAAAGTGTGTTTCAAGGC 2215  
 QY 701 TyrLysAsnTyrPheArgAlaGlyAlaHisTyrIleValPheIlePheLeuIleLeuLeu 720  
 Db 2216 TATAAGAAATTACTTCAGAGCTGTGTCTCACTGATGTCTTCAATTTTCTTATTTCTCTTA 2275

QY 721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTyrTyrPheSerTyrTyrAlaAsn 740  
 Db 2276 AACACTGACGCTCAGGTGGCTGATATGTCTTCAAGATTTGTGGCTTTCATCTGGCGCAAC 2335  
 QY 741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyGlyAsnValThrGluLysLeuAsp 760  
 Db 2336 AAACAAAGTATGCTTAATGTCACTGTAAATGAGAGGAATGTAAACCGAAGACTAGAT 2395  
 QY 761 LeuAsnTyrTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780  
 Db 2396 CTTAACTGTACTTAAGAAATTTATTCAGGTTTAACTGATGACCGGTTCTTTTGGCATTA 2455  
 QY 781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800  
 Db 2456 GCAGATCTCTATTTGTATTTCTACGCTCTTGTAACTTTCAACAACTTTGCAACAACAA 2515  
 QY 801 MetPheGlnSerIleLeuLysAlaProValLeuPheAspArgAsnProIleGlyArg 820  
 Db 2516 ATGTTTGAAGTCAATTTGAAAGCTCGGTTATTTATTTGATGAAATCCAATAGGAAGA 2575  
 QY 821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840  
 Db 2576 ATTTTAAATCGTTTCTCCAAAGACATTCGACACTTGATGATTTGCTGCGCTGACGTTT 2635  
 QY 841 LeuAspPheIleGlnThrLeuGlnValValGlyValAlaSerValAlaValAlaVal 860  
 Db 2636 TTAGATTTCAATCCAGACATGTGTACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2695  
 QY 861 IleProTyrIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880  
 Db 2696 ATTCCTTGATCGCAATACCTGCTGCTCCCTGGAATCATTTTCAATTTTCTTGGGGA 2755  
 QY 881 TyrPheLeuGlnThrSerArgAspValLysArgLeuGlnSerThrThrArgSerProVal 900  
 Db 2756 TATTTTGGAAACCTCAAGAGATGTGAAGCCCTGGAATGTACAACTCGAGTCCAGTG 2815  
 QY 901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTyrTyrIleArgAlaTyrLysAlaGlu 920  
 Db 2816 TTTTCCACTGTGCAATCTTCTCTCCAGGGGCTGTGACATCCGGGCAATCAACAGCAAA 2875  
 QY 921 GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGlyAlaTyrPheLeu 940  
 Db 2876 GAGAGTGTCAAGAACTGTTGATGACACACAGAAATTAACATTCAGAGGCTTGTTCTTG 2935  
 QY 941 PheLeuThrThrSerArgTyrPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960  
 Db 2936 TTTTGAACAACGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2995  
 QY 961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980  
 Db 2996 ATCATGCTTGCTTGGGTGCTCTGATTTGTGCAAAACCTGGAAGCCGGGAGGTTGTGT 3055  
 QY 981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTyrCysValArgGlnSer 1000  
 Db 3056 TTGGACGTCTCTAAGCCCTCAAGCTCAATGGGAATGTTTCACTGTGTGTGTGCAAAAGT 3115  
 QY 3116 GCTGAAGTTGAATATATGATGATCTCACTAAGAGGTCATTTGAATACACAGACTTGA 3175  
 QY 1021 LysGluAlaProTyrGluTyrGlnLysArgProValAspTyrProHisGlnGlyVal 1040  
 Db 3176 AAAGAAAGCACTTGGAATATCAAGAAAGCCACACAGAGCTGGCCCCATGAAGAAAGT 3235  
 QY 1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060  
 Db 3236 ATTAATCTTGACAAATGTAATCTCATGTACAGTCCAGGTGGGCTCTGTGTCTGAAGAT 3295  
 QY 1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyAlaGly 1080  
 Db 3296 CTGACAGCACTCAATTAATCAAGAAAGAGGTGTCATTTGGGAAAGAAACCGAGCTGGA 3355



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QY 1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGluLysIleTrrpIle 1100
DB 3356 AAAAGTTCCTCATCTCAGCCCTTTTATGATTTGTCAAGAACCGAAGGTAATTTGGANT 3415
QY 1101 AapLysIleLeuThrThrGluIleGlyLeuHlsAapLeuArgLysLysMetSerIleIle 1120
DB 3416 GATAGATCTTGACAACTGAATAATGACCTTCAAGATTAAAGAGAAATGCAATCAATA 3475
QY 1121 ProGluGluProValLeuPheThrThrThrThrMetCArgLysAsnLeuAapProPheAsnGlu 1140
DB 3476 CCTCAGGAACCTGTTTGTTCCTGACGAAACATGAGAAACCTGGATCCCTTTAAAGAG 3535
QY 1141 HisTrpAspGluGluLeuTrpAsnAlaLeuGluGluValGluLeuLysGluThrIleGlu 1160
DB 3536 CACAGGATGAGAGAACTGTGGAATGCTTACAAGAGGTCAACTTAAAGAAACCAATTGA 3595
QY 1161 AapLeuProGluLysMetCAspThrGluLeuAlaGluSerGlySerAsnPheSerValGly 1180
DB 3596 GATCTTCCCTGTTAAATGATGATCTGAATTAAGCAGATCCCAATTTTGTGTGGA 3655
QY 1181 GluArgGluLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGluIleLeuIleIle 1200
DB 3656 CAAAGCAACTGCTGTGCTTCCAGGAGCAATTTCTCAGAAATATCAGATTTGATTAT 3715
QY 1201 AapGluAlaThrAlaAsnValAapProArgThrAapGluLeuIleGluLysLysIleArg 1220
DB 3716 GATGAAGCAGCGCAAAATGTGATCCAAAGACTGATGATTATACAAATAATCCGG 3775
QY 1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAap 1240
DB 3776 GAGAAATTTGCCACGACCGCTGCTAACCATTTGCAACAGATTTGAACCACTTTATGAC 3835
QY 1241 SerAspLysIleMetCValLeuAapSerGlyArgLeuLysGluLysAspGluProTyrVal 1260
DB 3836 AGCGACAAATATGTTAGTTTATGATTCAGAAAGCACTAAAGAAATATGATGACCGTATGT 3895
QY 1261 LeuLeuGluAsnLysGluSerLeuPheTyrLysMetCValGluGluLeuGlyLysAlaGlu 1280
DB 3896 TTGCTGCAAAATTAAGAGAGCCCTATTTTCAAGATGTGTCACCAACTGGGCAAGCAGAA 3955
QY 1281 AlaAlaAlaLeuThrGluThrAlaLysGluValTyrPheLysArgAsnTyrProHisIle 1300
DB 3956 GCGCGCCCTCCTCACTGAAACAGCAAAACAGGATATCTTCAAAAGAAATTAATCCACTAT 4015
QY 1301 GlyHisThrAspHisMetCValThrAsnThrSerAsnGlyGluProSerThrLeuThrIle 1320
DB 4016 GGTCACTGACCACTGCTGTTACAAACACTTCCAAATGACAGCCCTCGACTTAATCTAT 4075
QY 1321 PheGluThrAlaLeu 1325
DB 4076 TTCAGACAGCACTG 4090

```

## RESULT 15

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ADR66822
ID ADR66822 standard; DNA; 5832 BP.
XX
AC ADR66822;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human prostatic carcinoma derived DNA SEQ ID 115 #4.
XX
KW human; cytostatic; diagnosis; prostatic cancer;
XX differential expression analysis; ds.
XX
OS Homo sapiens.
XX
PN WO2004076614-A2.
XX
PD 10-SEP-2004.
XX
PF 22-FEB-2004; 2004WO-DE000433.
XX

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PR 27-FEB-2003; 2003DE-01009965.
PR 14-MAY-2003; 2003DE-01022134.
XX
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
XX
PI Hinemann B, Dahl E, Rosenthal A, Hermann K, Pilarczyk C, Specht T,
PI Schmitt A, Beckmann G, Bruemendorf T, Kimmernann H, Roepcke S,
PI Kinxhong L, Staud E;
XX
PS WPI; 2004-653386/63.
XX
PT New nucleic acids, and encoded proteins, from prostatic cancer tissue,
PT useful for diagnosis, treatment and in screening for specific binding
PT agents.
XX
PS Claim 1; Page 1348-1349; 1607pp; German.
XX

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This invention describes novel cytostatic polynucleotide and polypeptide sequences which can be used in a method for diagnosing prostatic cancer or the risk of developing prostatic cancer. Diagnosis is based on determining over transcription or over expression of the sequences in prostatic tissue. Screening for inhibitors of the sequences or detection substances involves a binding assay, any compounds that bind are selected, optionally after deconvolution of mixtures. Detection of a predetermined minimum level of the reporter indicates the presence of tumor cells. Inhibitors can be chosen from antisense oligonucleotides, short-interfering RNA or ribozymes; an organic molecule of molecular weight below 5000, preferably 300, that binds to the polypeptide; an aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the polypeptide, preferably humanised or human; an anti-idiotypic, non-human (monoclonal) antibody directed against Ab or any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or radioisotope. The polynucleotides are identified in human prostatic cancer by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over)expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that CD24 was upregulated in many of them. Sections of tissue, isolated from prostatic cancer patients, or subjects at risk, were incubated sequentially with anti-human CD4 murine monoclonal antibodies; biotinylated second antibody; streptavidin-conjugated horseradish peroxidase and then diaminobenzidine as colour former (brown). The samples were counterstained with hemalum (blue). Malignant cells stained strongly but non-malignant cells only weakly. In 15 of 63 samples of adenocarcinoma, membrane and cytoplasmic staining was very strong, and lymph node metastases were also stained. ADR65805-ADR65954 represent the polynucleotide and polypeptide sequences used in the method of the invention.

Sequence 5832 BP; 1660 A; 1175 C; 1306 G; 1691 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	0	Length:	5832
Score:	6779.00	Matches:	1323
Percent Similarity:	99.9%	Conservative:	1
Best Local Similarity:	99.8%	Mismatches:	0
Query Match:	99.9%	Indels:	0
DB:	13	Gaps:	0

US-09-976-858-42 (1-1325) x ADR66822 (1-5832)

```

QY 1 MetLeuProValTyrGluGluValLysProAsnProLeuGluAsnAlaLeuCysSer 20
DB 116 ATGCTGCCCGTGTACAGAGAGGTGAAGCCCAACCGCTGACGAGACGCAATCTGCTCA 175
QY 21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40
DB 176 CGCGTGTCTTGTGTGCTCAATCCCTTTAAATTTGGCAAAACGAGATTAGG 235
QY 41 GluAapAapMetTyrSerValLeuProGluAapArgSerGluHisLeuGlyGluLeu 60

```

226 GAAAGATGATATGATATTCAGTGTCCAGAAAGCCGCTCAGACACCTTGAGAGAGATTG 295  
61 GINGUYPHEPTAPAPLYBSGLUVALLEUAAGLALAGLUASAPLALAGLULYSEPTLEU 80  
296 CAAGGATTCGGAGATTAAGAGATTTTAAAGCTGAGAAAGACGACAGAAAGCCCTCTTAA 355  
81 THRAGAALALIELYSECTYRTPLYSERTYRLEUVALLEUGLYLEPHEPTLEU 100  
356 ACAAGGACATCATTAAGTGTATCTGGAATCTTATTTAGTTTGGAAATTTTACGTTA 415  
101 ILEGUGUSERALYVALLEGNPROILEPHELEUGLYLSLEIASEANTYRPE 120  
416 ATTGAGAAAGTCCAAAGATTAATCCAGCCCATATTTTGGAAAATTAATTAATTTT 475  
121 GLUANTYRASPROMECASPERVALALALEUAERTHATYRALATYRALATHRAL 140  
476 GAAATATTAATGATCCATGATTTCTGTGCTTGAACACAGCGTACGCCCTATGCCAGG 535  
141 LEUTHRPHCYETHRLEULLEUALALILEUHLSELEUPTYRPHETRYHSAVALGIN 160  
536 CTGACTTTTGCACGCTCATTTTGGCTATACCTGATCATCTTAATTTTATCACTTCAG 595  
161 CYBALAGLYMECARGLEUARGVALAMECYSHIAMELIEYRARGLYSALALEUARG 180  
596 TGTGCTGGGATGAGGTACGAGTAGCATGTGCCATATGATTTATCGAAGGCACTTGT 655  
181 LEUSERAENMERALAMEGLYLYSTHRTTHRGILYGINLEVALLEUENLEUSERAN 200  
656 CTTAATACTNTGGCATGGGAAAGACACACAGGCCATAGTACATCTGCTGCCAT 715  
201 ASPVALAENLYSPHASPGLINVALTHRALPHELUHSPHELEUTRALAGLYPROLEU 220  
716 GATGTGAACAACTTTGATCAGGTGACAGTGTCTTAACCTTCTGGGACAGACACATG 775  
221 GINALALIALAVALTHRALALEUENUTRPMETGLULLEGLYLSERCYSEUVALAGLY 240  
776 CAGGAGATCGAGTAGTGCCTTACTCTGGATGAGATAGGAATTCGTGCTGTGG 835  
241 METALAVALLLEULIELLEUENUPROLEUGINSECYSPHEGLYLYLEUPHESERSE 260  
836 ATGGCAATCTATATCTCTCTGCCCTTGCAAGGTGTTTGGGAAGTGTTCATCA 895  
261 LEUATGSEPTLEUTHRALATHPHERHAPALATRGILYTHMETASNGILUVALILE 280  
896 CTGAGAGATTAACCTGCACTTTCACGAGATGCCAGATCAGACCATGATATAAGTTAA 955  
281 THRGILYLEARGILEILEYSECTYRALATRGILYLYSESPHESERANLEULIETHR 300  
956 ACTGATATAGATTAATAAATAATGTAACGCTGGAAAAGTCAATTTTCAAACTTAATTAC 1015  
301 AENLEUAAGLYLYSEGLULIESTERYLILEUAATGSESECYSEUARGLYMECAN 320  
1016 AATTGAGAAAGAAAGAGATTTCAGAGATTCGAGAAAGTTCCTGCTCAGGGGAGTAAT 1075  
321 LEUAIASERPHESERASERLASERYSLEILEVALPHEVALTHPHEHTRHTRTYRAL 340  
1076 TTGGCTGTGTTTTCAGTGCAAGCAAAATCATCGTGTGTGACCTTCCACCACTTACG 1135  
341 LEUENGLYSEVALILETHRALASERARGVALPHEVALALAVALTHREUTYRGLYALA 360  
1136 CTCCCTCGGAGTGTATCAGACGACGCGCTGCTGTGCGAGTACGCTGTATGGGGCT 1195  
361 VALAAGLEUTHRALTHREUPHESERVALILEGLUARGVALSERGLUALILE 380  
1196 GTGCGCTGACGGTTACCTCTTCTTCCCTCAGCATTAAGAGGGGTGCAAGGCAATC 1255  
381 VALSERILEARGILEGLINTHPHELEULEUAEPGLULIESTERINARGANARG 400  
1256 GTACACATCCGAAGATCCAGACCTTTTGTACTTGATGAGATATCAGAGGCAACGCT 1315  
401 GLINLEUPROSERASPGLYLYLYSECTVALHISVALGINASPHETHRALAPHEPTAP 420

1316 CAGCTGCCGATGATGTAAAAAGATGTGCATGTGCAGATTTTACTGCTTTTGGAT 1375  
421 LYSALASERGLUTHRPROTHLEUGINGLYLEUSERPHEHTRVALARGPROGLYGLILEU 440  
1376 AAGGATCAGAGAACCCCACTCTACAGGCCCTTCTTACTGTAGACCTGGCAATTG 1435  
441 LEUAIALVALAGLYPROVALGLYVALAGLYSESEPTLEUENLEUVALLEUGLY 460  
1436 TTAGCTGTGTGCGCCCTGGAGACAGAGATCATCATCTTTAAGTCCGCTCGGG 1495  
461 GLULEUALAPOSERHIEGLYLEUVALSERVALHISGLYARGILEALATYRVALSERGLIN 480  
1496 GAATGGCCCAAGACAGGCGCTGGTCAGCGTGCATGAGAAATGCTTATGTCTCAG 1555  
481 GLNPROTPVALPHESEGLYTHREUARGSERANILEUPHGLYLYLYSEPTYRGLU 500  
1556 CAGCCCTGGGTCTCGGAACTCTGAGATTAATTTTATTTGGAAAGAAATATGAA 1615  
501 LYSGLUARGTYRGLULYVALILEYBALACYSALALEULYLYSPLEUGINLEUEN 520  
1616 AAGGACATATGAAAAAGTCAATTAAGCTTGTCTGAAAAGATTTTACAGCTGTG 1675  
521 GLUASPGLYASPLEUTHRALILEGLYAPARGGLYTHRTHEUSERGLYGLINLYS 540  
1676 GAGGATGGTGAATCTGATCTGATAGAGATCGGGGAAACAGCTGAGTGAAGGCAAAA 1735  
541 ALAARGVALAENLEUALAARGVALATYRGINASAPLALAPLILETYRLEUENASAP 560  
1736 GACGAGGTAAACCTTGCAAGAGAGGTATCAAGATGTGACATTAATCTCTGACGAT 1795  
561 PROLEUSERALAVASAPLALAGLUVALSERARGHISLEUPHGLULYCYSLIECYSGIN 580  
1796 CCTCTCATGCAATGATGACGAGACTGACAGACCTTGTGAACTGTATTTGTCA 1855  
581 ILEUHLISGLULYLETHRLILEUVALTHRHISGLINLEUGINTYRLEUVALALALA 600  
1856 AATTGATGAGAAAGATCACAAATTTAGTCACTCATGAGTACCTCAAACTGCA 1915  
601 SERGINILEULILEULYASAPGLYLYMECTVALGINLYSGLYTHRTTHRGILUPE 620  
1916 AGTCAGATTCGATTAATTAAGATGTAAATGTGCGAAGGGGACTTACCTGAGTTC 1975  
621 LEUYSERGLYILEASPHEGLYSEPTLEUENLYLYSPASAPENGLIUSERGLIN 640  
1976 CTAAATCTGTATATGATTTTGTGCTCTTTTAAAGAGATATGAGAAAGTAAACA 2035  
2036 COTCAGTTCCAGGAATCCCACTAAGATGTAACCTTCTCAGAGTCTTCGGTTGG 2095  
641 PROPROVALPROGLYTHRPROTHLEUARGANARGHTRPHESEGLUSERSEVALITP 660  
2096 TCTCAACATCTTCTGAGACCTCTCTGMAAGATGTGCTGAGAGCCAGCATATCAAG 2155  
661 SERGININSEPTARGPROSERLEUVALAPGLYALALEUGLUSERGLINAPHTRGILU 680  
2156 AATGTCCAGTTACCTATCAGAGGAAACGCTTCTGAAGAAAGTGTGTTTCAAGGCC 2215  
681 AENVALPROVALTHREUSERGLINLEUENARGSERGLIYLYVALAGLYPHEGLINLA 700  
2216 TATAAGATTAATCTCAGAGTGTGTGCTCATGAGATGTCTTCAATTTCTTATCTCTCA 2275  
701 TYRYSANTRYRPHARGALAGLYALAHISTPTILEVALPHEILEPHELEULILEUEN 720  
2276 AACACTGAGCTCAGGTGTCTATGTGCTTCAAGATGTGTGCTTCACTACGGCAAC 2335  
721 AENTRALALAGLINVALALATYRVALLEUGLNASPTPTPLSEPTTYRTPALAHEN 740  
741 LYSGLINSEPTLEUASVALTHRALASNGLYGLYASANVALTHRGILULYSELEUAP 760  
2336 AAACAAATATGCTTAATGCTCACTTAATGAGAGAAATGTACAGGAAAGTATGAT 2395  
761 LEUENITPTYRLEUGLYLETYRSEGLYLEUTHRALATARNVALLEUPHGLYILE 780  
2396 CTTAACGTACTAGAAATTAATTAAGTGAATTAATCTGAGTCAACGTTCTTTTGGCAT 2455

QY 781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800  
 DB 2456 GCAGAGATCTCTAATGGTATTTACGCTCTGTTAACTCTTCACAAACTTTCACAAACAA 2515  
 QY 801 MetPheGluSer11LeuLeuValProValLeuPhePheAspArgAsnPro11LeuLys 820  
 DB 2516 AAGTTTGAAGTCAATCTGAAAGCTCCGGATTAATCTTTGATGAAGAAATCCAAATAGAAAGA 2575  
 QY 821 11LeuAsnArgPheSerLysAsp11LeuGlyHisLeuAspAspLeuLeuProLeuThrPhe 840  
 DB 2576 ATTTTAAATCGTTTCTCCAAAGACATTTGAGACATTTGATGATTTGTCGCGCTGACGTTT 2635  
 QY 841 LeuAspPhe11LeuThrLeuLeuGlnVal1GlyValValSerVal1AspVal1AspVal 860  
 DB 2636 TTAGATTTTCATCCAGCATTTGCTACAGAGTGTGGGTGGTCTCTGTCGTGGCCGCGT 2695  
 QY 861 11LeuProPhe11Asp11LeuProLeuValProLeuGly11LeuPhe11LeuLeuArgArg 880  
 DB 2696 ATTTCTTGGATGCAATACCTTGGTCCCTTGGATCATTTTTCATTTTCTTGGCGCA 2755  
 QY 881 TyrPheLeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal 900  
 DB 2756 TATTTTGGAAACGTCAGAGATGTGAAGCCCTGGAATCTACAACTCGAGCTCAGTG 2815  
 QY 901 PheSerHisLeuSerSerSerSerLeuGlnGlyLeuTyrThr11LeuArg11AspLys11Glu 920  
 DB 2816 TTTTCCCACTTGATCTTCTCTCCAGGGGCTCTGGACATCCGGGCATACAAAGACAGA 2875  
 QY 921 GluArgGlyGlnGluLeuPheAsp11HisGlnAspLeuHisSerGlu11AspPheLeu 940  
 DB 2876 GAGAGGTGCAGAGACTGTTTATGACACAGAGATTTACATTCAGAGGCTTGGTCTTGG 2935  
 QY 941 PheLeuThrThrSerArgTyrPhe11Asp11LeuValArgLeuAsp111LeuCys11AspPheVal 960  
 DB 2936 TTTTGGACAACTCCGCTGGTCCGCTGCTGATGATCTGATGATCTGATGATCTGATGAT 2995  
 QY 961 11LeuVal11AspPhe11SerLeu11LeuVal11LeuVal11LeuVal11LeuVal11LeuVal 980  
 DB 2996 ATCATCGTTGCTGGTGGTCCCTGATTCGCGCAAAACTCTGAGTCCGGGAGGTGGT 3055  
 QY 981 Leu11AspSerTyr11AspLeuThrLeuMetGlyMetPheGlnTyrCysVal11ArgGlnSer 1000  
 DB 3056 TTGGCACTGTCTTAATGCTCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCA 3115  
 QY 1001 AlaGluVal11GluAsnMetMet11SerVal11GluArgVal11LeuTyrThrAspLeuGlu 1020  
 DB 3116 GCTGAAGTTGAGAAATATGATCTCAAGTGAAGGCTCATTTGAATACACAGACTTGA 3175  
 QY 1021 LysGluVal11ProTyrGluTyrGlnLysArgProProPro11Asp11ArgGluVal 1040  
 DB 3176 AAAAGAGCACCTTGGGAAATATACAGAAACGCCACACAGCTGGCCCATGAAAGAGTG 3235  
 QY 1041 11LeuPheAspAsnVal11AsnMetTyrSerProGlyGlyProLeuVal11LeuLysHis 1060  
 DB 3236 ATTAATCTTGAACAATGTGAATCTCAAGTCAAGTCCAGGTGGCTCTGTGTACTGAAGCAT 3295  
 QY 1061 LeuThr11Asp11LeuSerGlnGluLysVal11GlyVal11GlyVal11GlyVal11GlyVal 1080  
 DB 3296 CTGACAGCATCTTAATACACAGAAAGGTTGGCATTTGGGAGAAACCGAGCTGGA 3355  
 QY 1081 LysSerSerLeu11Ser11AspLeuPheArgLeuSerGluProGluGlyLys11LeuTyrPhe 1100  
 DB 3356 AAAAGTTCCCTCATCTCAAGCCCTTTTAATTTGATTTGTCAGAACCCGAGGTAAATTTGGATT 3415  
 QY 1101 AspLys11LeuThrThrGlu11LeuHisAspLeuArgLys11MetSer11Leu 1120  
 DB 3416 GATTAAGATCTTGAACAATGTGAATCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 3475  
 QY 1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140  
 DB 3476 CTTCAAGAACTGTGTTTTCATCTGAGAACATGAGGAAAACTGTGATCCCTTTAAGGAG 3535

QY 1141 HisThrAspGluGluLeuTyrAsn11AspGlnGluVal11GlnLeuLysGluThr11LeuGlu 1160  
 DB 3536 CACACGGATGAGGAATGTGTGAATGCTTTACAGAGGTATCAACTTAAGAAACCAATTGA 3595  
 QY 1161 AspLeuProGlyLysMetAspThrGluLeuVal11GluSerGlySerAsnPheSerVal11Gly 1180  
 DB 3596 GATCTTCTGTGTAATGATGATCTGAATTTACAGAAATAGGATCCAAATTTTATGTTGTA 3655  
 QY 1181 GlnArgGlnLeuVal11CysLeuVal11Arg111LeuVal11LeuVal11LeuVal11LeuVal 1200  
 DB 3656 CAAGACAACTGGTGTGCTTGCAGGGCAATTCACAGAAATAATCAGATATTTGATTAT 3715  
 QY 1201 AspGluVal11Thr11AsnVal11AspProArgThrAspGluLeu11LeuLysLys11LeuArg 1220  
 DB 3716 GATGAAGGACGGCAAAATGTGAATCCAGAACTGATGATTAATACAAAAAATAATCCGG 3775  
 QY 1221 GluLysPhe11HisCysThrValLeuThr11LeuHisArgLeuAsnThr11LeuAsp 1240  
 DB 3776 GAGAAATTTGCCCATGACCGGTGCTTAACATTTGACACAGATTTGACACCATTTAT 3835  
 QY 1241 SerAspLys11MetVal11LeuAspSerGlyArgLeuLysGluTyrAspGluProTyrVal 1260  
 DB 3836 AGCGACAAATATATGTTTATGATTCAGAAAGACTGAAGAAATATATGATGAGCGTATGTT 3895  
 QY 1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetVal11GlnGlnLeuGlyLysAsp11Glu 1280  
 DB 3896 TTGCTGCAAAATAAAGAGGCTTAATTTTACAAAGATGTGTGCAACAACTGGGCAAGGACAGA 3955  
 QY 1281 Ala11Asp11LeuThrGluThrAlaLysGlnVal11TyrPheLysArgAsnTyrProHis11Leu 1300  
 DB 3956 GCCGTGCCCTCAGTGAAGACGAAACAGGATTAATCTTCAAAAGAAATTAATCCACATTT 4015  
 QY 1301 GlyHisThrAspHisMetVal11ThrAsnThrSerAsnGlyGlnProSerThrLeuThr11Leu 1320  
 DB 4016 GGTCACTGACCAATGATGTTACAAACACTTCATGATGACAGCCCTGACCTTAATCTATT 4075  
 QY 1321 PheGluThr11Asp11Leu 1325  
 DB 4076 TTCGAGACAGCACCTG 4090

Search completed: March 14, 2006, 08:36:53  
 Job time : 1773 secs

GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 14, 2006, 08:37:01 ; Search time 1315 Seconds  
(without alignments)  
5478.823 Million cell updates/sec

Title: US-09-976-858-42

Perfect score: 6787

Sequence: 1 MLPVQEVKPNPLQDANLCS.....WVTNTSNGQPSLTITFETAL 1325

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODE=frame\_plus\_p2n.model -DEV=xlh  
-O=/abs/ABSSWEB\_spool/US09976858/runac\_13032006\_170101\_11806/app\_query.fasta\_1  
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=ab8808  
-USER=US09976858@CCN\_1\_1\_5315@runac\_13032006\_170101\_11806 -NCPU=6 -ICPU=3  
-NO\_WAP -NEC\_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST.\*  
1: gb\_esc1.\*  
2: gb\_esc2.\*  
3: gb\_esc3.\*  
4: gb\_hic.\*  
5: gb\_esc4.\*  
6: gb\_esc5.\*  
7: gb\_esc6.\*  
8: gb\_esc7.\*  
9: gb\_gsa1.\*  
10: gb\_gsa2.\*  
11: gb\_gsa3.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5864	86.4	4594	4 AK052778	Mus muscu
2	5553	81.8	3685	10 AY415506	Homo sapi
3	4828	71.1	3679	10 AY415508	Mus muscu
4	4395	64.8	3685	10 AY415507	Mus muscu
5	2582	38.0	3208	4 AK032802	Mus muscu
6	2263	33.3	5920	4 AK029876	Mus muscu
7	2216.5	32.7	5899	4 CR749835	Homo sapi

8	2144	31.6	4547	4 BC046560	Mus muscu
9	2138	31.5	4953	11 CL969772	OsRIFC018
10	2046.5	30.2	4638	11 DQ044660	Homo sapi
11	2043.5	30.1	4080	11 DQ038460	Homo sapi
12	1968.5	29.0	4185	10 AY407265	Homo sapi
13	1957.5	28.8	4176	10 AY407267	Mus muscu
14	1955	28.8	4483	10 CL957124	OsRIFC019
15	1942.5	28.6	4425	10 CL970490	OsRIFC019
16	1920.5	28.3	4185	10 AY407266	Homo sapi
17	1888.5	27.8	4452	10 CL968077	OsRIFC016
18	1883	27.7	4224	11 DQ049053	Homo sapi
19	1880	27.7	4425	10 CL963465	OsRIFC009
20	1861	27.4	4773	11 DQ045352	Homo sapi
21	1835.5	27.0	1655	4 CNG0568R	Tetradon
22	1822.5	26.9	1655	4 CNG0568R	Tetradon
23	1817	26.8	4161	10 CL952237	OsRIFC013
24	1813.5	26.7	3561	10 CL966129	OsRIFC013
25	1797	26.5	4443	10 AY399795	Homo sapi
26	1784.5	26.3	4686	10 CL969658	OsRIFC018
27	1781	26.2	4149	11 DQ038456	Homo sapi
28	1726	25.4	4542	10 AY412332	Homo sapi
29	1706.5	25.1	3588	10 CL964834	OsRIFC011
30	1697	25.0	4529	10 AY412334	Mus muscu
31	1688	24.9	3975	10 AY399797	Mus muscu
32	1682.5	24.8	4638	11 DQ044661	Homo sapi
33	1661.5	24.5	1493	4 CNG0568R	Tetradon
34	1657	24.4	3561	10 CL979509	OsRIFC013
35	1624	23.9	3597	10 CL966131	OsRIFC013
36	1536	22.6	4716	4 AK049174	Mus muscu
37	1520	22.4	4773	11 DQ045353	Homo sapi
38	1514.5	22.3	2397	10 CL958547	OsRIFC001
39	1507	22.2	4905	10 CL963549	OsRIFC009
40	1501	22.1	3361	4 AK083916	Mus muscu
41	1499.5	22.1	3174	11 DQ050048	Homo sapi
42	1455	21.4	4242	8 AY399796	Homo sapi
43	1317	19.4	1195	8 DN698293	Cluj16-G03
44	1250.5	18.4	4460	11 DQ030756	Homo sapi
45	1250	18.4	1084	3 BM462073	AGENCOURT

#### ALIGNMENTS

RESULT 1  
AK052778 4594 bp mRNA linear HTC 03-APR-2004  
LOCUS  
DEFINITION Mus musculus 0 day neonate kidney cDNA, RIKEN full-length enriched library, clone: D630049P08 product: ATP-binding cassette, gub-family C (CFTR/MRP), member 4 homolog (Human), full insert sequence.  
ACCESSION AK052778.1 GI:26095372  
VERSION  
KEYWORDS  
SOURCE HTC, CAP trapper.  
ORGANISM Mus musculus (house mouse)  
MUS musculus

#### REFERENCE

REFERENCE  
AUTHORS Carninci, P. and Hayashizaki, Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
PUBMED 10349636  
REFERENCE  
AUTHORS

#### TITLE

JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komoto, H., Akiyama, U., Nishi, K., Kitanai, T., Tashiro, H., Itoh, M., Sun, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kaishiwagi, K.,



QY 385 ArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArgIleuProSer 404  
 Db 1246 AGGATCAAGAACTTCTTACTGATGATACACAGCGCAAGCCCATGATACATCT 1305  
 QY 405 AspGlyIleValMetValIleValGlnAspPheThrAlaPheTrpAspLysAlaSerGlu 424  
 Db 1306 GATGGCAAGCAATGTCCAGTCGACAGATTTCACCGCTTCTGGGACAGGCACTAGAC 1365  
 QY 425 ThrProThrIleuGlnGlyLeuSerPheThrValAlaProGlyGlyIleuLeuAlaValAla 444  
 Db 1366 AGTCACACCTCGCAAGGCTCTTCTTATTCGACAGCGCTGGAGATTGTGTAGCCCTGGTT 1425  
 QY 445 GlyProValGlyAlaGlyIleSerSerLeuLeuSerAlaValIleuGlyGlyIleuAlaPro 464  
 Db 1426 GGGCCAGTTGGAGCGCAAGTCGCTGCTTGAAGAGAGCTGCGTGGAGCTGCTCTCT 1485  
 QY 465 SerHisGlyLeuValSerValHisGlyValArgIleAlaIleValSerGlnGlnProTrpVal 484  
 Db 1486 GCCAGCGGGCTGTCAGCGGTGACGGGAGATCGCTTACGTTTCTCACAGCGCTGGGTG 1545  
 QY 485 PheSerGlyIleThrLeuArgSerAsnIleLeuPheGlyIleValGlyIleValGlyIleVal 504  
 Db 1546 TTCTCGGCGCACCGTAGAGCAATATTTATTTGGAAAGAAATATGACAGAGGAGCATAT 1605  
 QY 505 GluIleValIleIleValAlaCysAlaLeuLysLysAspLeuGlnIleuLeuGluAspGlyAsp 524  
 Db 1606 GAGAAAGTATCAAGGCTGTCGCTTGAAGAGAGCTGCACTTCTGAGAGAGCGGGAT 1665  
 QY 525 LeuThrValIleGlyAspArgGlyIleThrLeuSerGlyGlyIleValAlaArgValAsn 544  
 Db 1666 CTGACGCTTATAGAGACCGGGAGACCAAGCTGAGAGGCGCAAGAGCTGGGTGAC 1725  
 QY 545 LeuAlaAlaGlyAlaValIleGlnAspAlaAspIleIleValLeuAspAspProLeuSerAla 564  
 Db 1726 CTGGACCGGCGCTGTACAGAGCCGCAACATCTCTCTTGAAGATCCGCTGACCGCT 1785  
 QY 565 ValAspAlaGlyValSerArgHisLeuPheGlyIleuValCysValIleLeuHisGly 584  
 Db 1786 GTGATGAGAGAGTGGGCAAGAGCTGTTCACACTGTGTATGTGACGCGCTTGACAG 1845  
 QY 585 LysIleThrIleLeuValIleThrHisGlnIleuGlnIleValAlaAlaSerGlnIleLeu 604  
 Db 1846 AAGATCACATTTTATGTGATCAGCAAGTTTACGTTTCAAGGTCGCAAGGCAACATCTCT 1905  
 QY 605 IleLeuLysAspGlyIleValMetValGlnLysGlyIleThrIleGlnPheLeuLysSerGly 624  
 Db 1906 ATACTCAAGATGTGTGAGATGTGTGCAAGAGGAGCTTACACGAGTTTCTGAAATCTGT 1965  
 QY 625 IleAspPheGlySerLeuLeuLysLysAspAsnGlyIleuGlnProProValPro 644  
 Db 1966 GTAGATTTTGGCTCCCTGTTAAAGAAAGAAAGAGAGAGAGAGCCCTCCACAGCCCA 2025  
 QY 645 GlyThrProThrIleuArgAsnArgThrPheSerGlyIleuSerValTrpSerGlnIleuSer 664  
 Db 2026 GGAACCCCGACACTCAGGAAAGCAACTTCTCCGAGGCTCAATTGGTCTCAGAGTCA 2085  
 QY 665 SerArgProSerLeuLysAspGlyAlaLeuGlyIleuSerGlnAspThrGlnAsnValProVal 684  
 Db 2086 TCCAGACCTTCCTGTAAGAGCGGGGCCCGACAGGCGCAAGAGAGAGAGCAACGAGGCA 2145  
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REFERENCE 1 (bases 1 to 3685)  
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejaritwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civeallo,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE gene ttrios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 3685)  
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejaritwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civeallo,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J.,  
Adams,M.D. and Cargill,M.

TITLE Direct Submission  
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 1 (bases 1 to 3679)  
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 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous

JOURNAL gene tribes  
 Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 3679)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,  
 Adams,M.D. and Cargill,M.  
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 Db: 10 Gaps: 1  
 US-09-976-858-42 (1-1325) x AY415508 (1-3679)  
 Qy 63 PheTrpAspLysGluValIleuArgAlaGluAsnAspAlaGlnLysProSerLeuThrArg 82  
 Db 2 TACTGGATTAAGAAGCTTCTGAGGCCAAGAAGACTGAGAGAAGCCCTCTTAAAGAAAG 61  
 Qy AAlaIleIleYsCysYrTrpLysSerYrLeuValLeuGlyIlePheThrLeuIleGlu 102  
 Db 62 GCATCATTAAGAAGTGTACTGAGAAGCTTACCTGATTTGGGAATTTTACCTTAATTAG 121  
 Qy 103 GluSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnYrPheGluAsn 122  
 Db 122 GAGGCGACTCGAGATGATCAGCCCTTATTTTAAAGAAATTAATTAATTTTGAAGAG 181  
 Qy 123 TyrAspPrometAspSerValAlaLeuAsnThrAlaYrAlaYrAlaThrValLeuThr 142  
 Db 182 TATGACCCGAGACACTCGGTGGCTTTCATACAGCTTATGGCTACGACAGCTGCTGCC 241  
 Qy 143 PheCysThrLeuIleLeuAlaIleLeuHisIleLeuYrPheYrHisValGlnCysAla 162  
 Db 242 ATGTGACGATCATCTGCGCATACATCATGATTTGATCTTACACAGTGCAGTGCAGC 301  
 Qy 163 GlyMetArgLeuArgValAlaMetCysHisMetIleYrArgLysAla-LeuArgLeuSe 182  
 Db 302 GGGATGAGCGTCGGGGTTCGATGTGCCATGATTTAC-----CNNNNNNNNNNNNNN 355  
 Qy 182 AsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsnAspVa 202  
 Db 356 NNN 415  
 Qy 202 LasnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeuGlnAl 222  
 Db 416 NNN 475  
 Qy 222 AlaLeuAlaThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGlyMetAl 242  
 Db 476 CATCGCGTTAACCGTCTCTCTGTGGTGAAGATGAAATCTCCCTGGCGGGCTGGC 535  
 Qy 242 aValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSerLeuAr 262  
 Db 536 CATTCTGGTATTCTTCTGCTCTCTGCAAGCTGCATCGGAAGCTGTTCTCTCCTACCTGG 595

QY 262 gserlyethralatrnphethraspalaargilleargthrmecAangluValillethrcgl 282  
 Db 596 GAGTAAACTGGCGCTTTCACGAGATCCGAGATCCGAGATCGAATGAAGTAAACAG 655  
 QY 282 ylleargillelleymetTyrAlaTrpGluysSerPheSerAenleullethrasnle 302  
 Db 656 CATGAGATGAATAAAGATGTATGCGTGAGAAATCGTTGCTGACCTCATTTGCCAATCT 715  
 QY 302 uarglyslvsglulleseylvalilleuabrgserCyseuarggllymetAenleu 322  
 Db 716 GAGAAAGAAAGAGATTTCCAGATTTCTGGGCACTCTCACTCAAGAGGATGAACATGCG 775  
 QY 322 aserPhePheSerAlaserlyleillevalPheValThrPheThrThyValleu 342  
 Db 776 GTTCGTTTTTCATCGGAACAAAGTCACTCTGTTGACCTTCACTAGTACTGCTGCT 835  
 QY 342 uGlySerValillethralaserArgValPheValAlaValThrleuYrGlyValaValar 362  
 Db 836 TGGCAATGAGATTAACAGTACGACCGTGTGTGGCCATGACTGTATCGGTGCGTTG 895  
 QY 362 gleuthrValThrleuPhePheProSerAlailegluargValaserGluAlailevalse 382  
 Db 896 GTTGACATGACCTCTCTCTCTCTCCGTCAGCCATTAGAGAGGGTCAAGGCCATGTCAG 955  
 QY 382 rilleargrilleglinThrPheleuLeuaspGluileserGlnArgAsnArgGlnle 402  
 Db 956 CATTCGAGAGATCAAGAACTTCTGTACTGATGAATCAACACAGCCGAAAGCCCATCT 1015  
 QY 402 uproSeraspGlylyslvmetValilevalGlnaspPheThrAlaPheTrpAspLysAl 422  
 Db 1016 ACCATCTAGTGGCAAGCATATGTCACGTCGAAATTTCAACGCTTCTGGGACAAAGCG 1075  
 QY 422 aserGluThrProThrleuGlnGlyleuSerPheThrValaArgProGlyGluLeuAla 442  
 Db 1076 ACTMAACGTCCACCCCTGCAAGGTCCTTCTTATTCGCAACCTGTGAGATTTGTAGC 1135  
 QY 442 aValValGlyProValGlyAlaGlyLysSerSerleuSerAlaValleuGlyGlnle 462  
 Db 1136 CGTGTTGGCCAGTTCGAGCGAGCGAAGTCGTGCTGTTGAGCGAGTCTGGGTGAGCT 1195  
 QY 462 uAlaProSerHisGlyleuValSerValHisGlyValArgillealalyValaserGlnGln 482  
 Db 1196 GCCTCTCCACGCGGGCTGTGTGACGTGCAACGAGAGATCGCTAGTTCTCACAGCGC 1255  
 QY 482 cTrpValPheSerGlyThrleuArgSerAenleulleuPheGlylyslvYrGlyLysGln 502  
 Db 1256 CTGGGTGTTCTCGGACCGTGAAGAGCAATATTTATTTGGGAAATATGAAAGAGA 1315  
 QY 502 uArgTrpGluysValilleysAlaCyallaleuylslvAspLeuGlnleuLeuGluAs 522  
 Db 1316 GCGATATGAGAAAGTATGATCAAGGCTGTGCTCTGAAGAGAGACCTTGACCTTCTGAGGA 1375  
 QY 522 pGlyAspLeuThrValilleGlyAspArgGlyThrThrleuSerGlyGlyGlnlyAlaAr 542  
 Db 1376 CGGGATCTGACGGTTATAGAGACCGGGGAGCCACGCTGAGTGAAGGCAAGAAAGCTCG 1435  
 QY 542 gValAenleuAlaArgAlaValTrpGlnAspAlaAspIleTrpLeuLeuAspAspProle 562  
 Db 1436 GGTGAACCTGGACCGGCGCTTACACAGACCGCCACATCACTCTTGAAGATCCGCT 1495  
 QY 562 uSerAlaValAspAlaGluValaserArgHisleuPheGluLeuCyseileCyseGlnIlele 582  
 Db 1496 CAGCGCTGTGATGAGAGAGTGGCAAGCACTGTTCACACTGTATCTGTCAAGCGCTT 1555  
 QY 582 uHisGluYslleThrilleuValThrHisGlnleuGlnTrpLeuYslAlaAlaserGln 602  
 Db 1556 GCACAGAGAAAGATCAACATTTAGTACTCACCAAGTTACAGTACTCAAAAGCTGCAAGCCA 1615  
 QY 602 nIleleuIleleuysAspGlylyslvmetValGlnlyslvYrThrTrpGlnPheleu 622  
 Db 1616 CATCTCTACTCAAGAGATGTGAGATGTGCAAGAGGGGACTTTCACAGGAATTTCTGA 1675  
 QY 622 sserGlylleasPheGlySerleuLeuylslvAspAenGluGlnSerGluGlnProPr 642

Db 1676 ATCTGTGTAGATTTTGGCTCCCTGTAAAGAAAGAAACAGAGAGAGCCCTCCAC 1735  
 QY 642 oValProGlyThrProThrleuArgAsnArgThrPheSerGlnSerValTrpSerGln 662  
 Db 1736 AGCCCAAGAAACCCCGACACTCAGGAAACGAACCTTCTCCGAGGGCTCAATTTGGTCTCA 1795  
 QY 662 nGlnSerSerArgProSerleuLysAspGlyValaleuGlnSerGlnAspThrGluAsnVal 682  
 Db 1796 GCAATCTCAAGACCTCTGTGAAGAGCGGGCCCCAGAGGGCCAAAGCGCAAGAAACAC 1855  
 QY 682 lProValThrleuSerGlnGluAsnArgSerGlnGlylyslvAlaGlyPheGlnAlaTrp 702  
 Db 1856 GCAGGCACTGCAACCCGAGAGAGCGCTTCGAGAGGAGAAATCGGCTTCAAGGCTTACAA 1915  
 QY 702 sAsnTrpPheArgAlaGlyAlaHisTrpIleValaPheleuLeuIleuLeuAsnTh 722  
 Db 1916 GAATTAATCTTCGCGGGCGCATCTGTGTTCTTCATCTTTCCTTGTGCTGTAAAT 1975  
 QY 722 rAlaAlaGlnValAlaTrpValleuGlnAspTrpTrpLeuSerTrpTrpAlaAsnLysGln 742  
 Db 1976 GGTGGCCAGGTTTCTATGTTCTTCAGAGACTGTGGCTTCCACTGGCGCAACAGCA 2035  
 QY 742 nSerMetLeuAsnValThrValAsnGlyGlylyslvAsnValThrGluysleuAspLeuAs 762  
 Db 2036 AGGTGCACTGAACAACACAGAAATCGAAATGGAATTAACGAGAACCTTAGACTCAG 2095  
 QY 762 nTrpTrpLeuGlylyleYrSerGlyLeuThrValAlaThrValleuPheGlylyAlaAr 782  
 Db 2096 CTGTACTTGAAGATTTACGAGAGTCTAACGCGGTCAACGCGTCACTTTTGGCATAGCGAG 2155  
 QY 782 gSerleuLeuValPheTrpValleuValAsnSerSerGlnThrleuHisAsnLysMetPh 802  
 Db 2156 ATCCCTAGTGGTGTATATCTTGTGAAGCTTCCAGACTTTCACACAGAGATGTT 2215  
 QY 802 eGlnSerIleleuLysAlaProValleuPhePheAspArgAsnProIleGlyArgIlele 822  
 Db 2216 TGAAGTCATAGAAAGCTCCCGTGTCTTCTTGACAGAAATCCAAATCGGAGAGATTTT 2275  
 QY 822 uAsnArgPheSerlyslvAspIleGlyHisleuAspAspLeuProleuThrPheLeuAs 842  
 Db 2276 AAATGTTTCTCAAAAGACATCGACATGATGATCACTGCTCCCTGACGTTCTCGA 2335  
 QY 842 pHeIleGlnThrleuLeuGlnValValGlyValaserValAlaValAlaValAlaIlePr 862  
 Db 2336 CTTCATCCAGAGTGTCTCTCGCTGAAGTGAATCCGTGTGCGCGCGCGCTGATCCC 2395  
 QY 862 cTrpIleAlaIleProleuValProleuGlyIleIlePheIlePheleuArgArgTrpPh 882  
 Db 2396 TTGATCTCATACATTCATTCGCTCCGCTTCAGTGTCTTCTGTTCTTCGAGATACTT 2455  
 QY 882 eLeuGlnThrSerArgAspVallyslvArgLeuGlnSerThrThrArgSerProValPheSe 902  
 Db 2456 CTTAGAGAGAGTCAAGGATGTCAAGCGCTCGAATCCAC-ACACGAGACCGCGTATTCTC 2514  
 QY 902 rHisleuSerSerSerleuGlnGlyleuThrThrIleArgAlaTrpYslAlaGlnGluAr 922  
 Db 2515 CCATTTATGTCCTCTCCACAGGACTTGAACCACTCGGGCTTCAAAAGCTGAGAGAG 2574  
 QY 922 gCyseGlnGluPheAspAlaHisGlnAspLeuHisSerGlnAlaTrpPheleuPhele 942  
 Db 2575 GTGTCAAGAGCTGTTTATGACACACAGCACTTCGATTCACAGAGCTTGTTCTTCTCT 2634  
 QY 942 uThrThrSerArgTrpPheAlaValaArgLeuAspAlaIleCyAlaMetPheValIleI 962  
 Db 2635 GACGACATCGAAGATGTGTGCTGTGCGTCTGAAGCGCCATCGCCCATCTTGTTCATCTG 2694  
 QY 962 eValAlaPheGlySerleuIleleuAlaValaThrleuAspAlaGlyGlnValaGlyleuAl 982  
 Db 2695 CGTGTCTTGGGCTCTGTGTTCTGGCAACATTTGATCTGGGAGGTGGCTGGC 2754  
 QY 982 aleuSerTrpAlaLeuThrleuMetGlyMetPheGlnTrpCyValaArgInserAlaGln 1002

Db	2755	CTTGTCTCAGCCCTCACACTCAGGGGATTTCCAGATGGTCTGTGGACAGAGCGCGCA	2814
Qy	1002	uValGluabnMetEclIleSerValGluabValIleGluTyrThrAspLeuGluYsgI	1022
Db	2815	AGTGAAGAATATGATGATTTTCAGTGGAGAGATGATTGACACGCACTTAGAAGA	2874
Qy	1022	uAlaProGluIuYrGluIuYsAyrProProAlaThrProHleGluGluValIleI	1042
Db	2875	GGCCCTTGGAGTGCAGAAAGCGCCACCCCGCTGGCCCAAGGGAGTCACTGT	2934
Qy	1042	ePheAspAsnValAsnPhemEtyrSerProGluYglYProLeuValLeuYshIleuth	1062
Db	2935	CTTGACAAATGTGAACCTTCACTACAGTTAGATGGGCTCTGGTTGAAAGCACTGAC	2994
Qy	1062	rAlaLeuIleIySergInGluYsValGlyIleValGlyArGthrGlyAlaGlyYsE	1082
Db	2995	TGCCCTCATCAAGTCAGGAAAAAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	3054
Qy	1082	rSerLeuIleSerAlaLeuPheAyrGleuSerGluProGluIuYsIleTrrIleAspIy	1102
Db	3055	NN	3114
Qy	1102	sIleuthrThrGluIleGlyLeuHleAspLeuAryIlySylMetSerIleIleProG	1122
Db	3115	NN	3174
Qy	1122	nGluProValLeuPheThrGlyIyrMetArGlyAsnLeuAspProPheangIuHle	1142
Db	3175	NGAACCTGTCTGTTCACATGGAACCATGAGAAAACTGGACCCCTTCATGTAGCAC	3234
Qy	1142	rAspGluIuLeuTrrPheAlaIleuGInGluValGluIleuYsgIuThrIleGluAspIe	1162
Db	3235	GGACGAGAGCTGTGGAGGGCTTGGAGAGAGTACACTTAAAGAGGCATTGAAAGTCT	3294
Qy	1162	uProGlyIySmetAspThrGluLeuAlaGlySerGlySerAsnPheserValGlyGlnAr	1182
Db	3295	TCCTGAAAAATGGATCTGATTCGATTCGACGAATCTGATTCGATTCGATTCGACGAG	3354
Qy	1182	gGluLeuValCysLeuAlaArGAlaIleLeuArGlySangInIleuIleIleAspG	1202
Db	3355	ACAGTTAGTGTCTTGGCAAGGGCCATCTTAAAGAAATACCGAATACATGATTCATGATGA	3414
Qy	1202	uAlaThrAlaAsnValaAspProArGThrAspGluLeuIleGluYsYsIleArGlyIuY	1222
Db	3415	AGCAACTCAATGTGGAAGCCCAAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	3474
Qy	1222	sPheAlaHleCysThrValLeuThrIleAlaHleArGLeuAsnThrIleIleAspSerAs	1242
Db	3475	NN	3534
Qy	1242	pLysIleMetValLeuAspSerGlyArGLeuYsgIuYrAspGluProYrValLeuLe	1262
Db	3535	NN	3594
Qy	1262	uGluAsnYsgIuSerLeuPheTyrIlyMetValGInGluIleuGlyIySAlaGluAlaI	1282
Db	3595	GCAGATCCAGAGACCTCTTTACAAATGTGTTCAGCAACTGGGCAAGGGCGAAGCGCG	3654
Qy	1282	aAlaLeuThrGluThrAlaIyGlnI	1290
Db	3655	TGCCCTCACGAAACGCAAAACAG	3679
RESULT 4			
AY415507			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;			

[illegible]

QY	223	Lea aVal Thr Ala Leu Leu Trp Met Glu Ile Gly Ile Ser Cys Glu Ala Gly Met Ala	242
Db	462	ATCGCAGGACGACGCCCTTNNNNNNNATGAGGAATGGAATATCGTCCTGGCTGGATGGCA	541
QY	243	VAlleu Ile Leu Leu Pro Leu Gln Ser Cys Phe Gly Leu Phe Ser Ser Leu Arg	262
Db	542	GTTCTATCATCTCTCTGCTTGCCTTGCAAGCTGTTTGGAAAGTTGTTCTTCAATCACTGAGG	601
QY	263	Ser Ly Ser Thr Ala Thr Phe Thr Asp Ala Arg Ile Arg Thr Met Asn Glu Val Ile Thr Gly	282
Db	602	AGTAAACACTGCAACTTTCACGGATGCGACAGATCAGGACCATGAAATGAAGTTATTAACGTGT	661
QY	283	Ile Arg Ile Ile Leu Met Thr Ala Trp Glu Lys Ser Phe Ser Asn Leu Ile Thr Asn Leu	302
Db	662	ATTAAAGATTAATTAATAATGATACGCCCTGGGAAAGATCATTTTCAAACTTATTTACCAATTGG	721
QY	303	Arg Ly Lys Glu Ile Ser Lys Ile Leu Arg Ser Ser Cys Leu Arg Gly Met Asn Leu Ala	322
Db	722	AGCAAAANNN	781
QY	323	Ser Phe Phe Ser Ala Ser Lys Ile Ile Val Phe Val Thr Phe Thr Thr Val Leu Leu	342
Db	782	NN	841
QY	343	Gly Ser Val Ile Thr Ala Ser Arg Val Phe Val Ala Val Thr Leu Trp Gly Ala Val Arg	362
Db	842	NN	901
QY	363	Leu Thr Val Thr Leu Phe Phe Pro Ser Ala Ile Glu Arg Val Ser Glu Ala Ile Val Ser	382
Db	902	NN	961
QY	383	Ile Arg Arg Ile Gln Thr Phe Leu Leu Leu Asp Glu Ile Ser Gln Arg Asn Arg Gln Leu	402
Db	962	NN	1021
QY	403	Pro Ser Asp Gly Lys Lys Met Val His Val Gln Asp Phe Thr Ala Phe Trp Asp Lys Ala	422
Db	1022	CCGTCAGATGGTAAAGATGGTGCATGGCGAGGATTTTATTCGCTTTTGGGATTAAGCA	1081
QY	423	Ser Glu Trp Pro Thr Leu Gln Gly Leu Ser Phe Thr Val Arg Pro Gly Glu Leu Leu Ala	442
Db	1082	TCAGAGACCCCACTCTACMAAGCCCTTCTCTTACTGTCAGACCTGCGCAATTTGTTAGCT	1141
QY	443	Val Val Gly Pro Val Gly Val Gly Lys Ser Ser Leu Leu Ser Ala Val Leu Gly Glu Leu	462
Db	1142	GTGGTCGGCCCGCTGGGAGCAGGAGAATCATCACTGTAAGGCCGTGCTCGGAGGAATTG	1201
QY	463	Ala Pro Ser His Gly Leu Val Ser Val His Gly Arg Ile Ala Ile Trp Val Ser Gln Pro	482
Db	1202	GCCCCAAGTCACGGCGCTGGTCAGCGTCATGAGAAATGGCTTATGTGTCTGACGAGCCC	1261
QY	483	Trp Val Phe Ser Gly Thr Leu Arg Ser Asn Ile Leu Phe Gly Lys Lys Ile Trp Glu Lys Glu	502
Db	1262	TGGGTTGTTCTCGGGAACCTGTGAGAGTAAATTATTTATTTGGGAAATAATCAAAAAAGAA	1321
QY	503	Arg Trp Glu Lys Val Ile Lys Ala Cys Ala Leu Lys Lys Asp Leu Glu Leu Leu Glu Asp	522
Db	1322	CGATATGAAAAAGATCATAAAGCTTGTGCTGCGAAAAAGNNNNNNNNNNNNNNNNNNNNNNNN	1381
QY	523	Gly Asp Leu Thr Val Ile Gly Asp Arg Gly Thr Thr Leu Ser Gly Gly Glu Lys Ala Arg	542
Db	1382	NN	1441
QY	543	Val Asn Leu Ala Arg Ala Val Trp Gln Asp Ala Asp Ile Trp Leu Leu Asp Asp Pro Leu	562
Db	1442	NNNNNNNNNNNNNNNAGCAGTGTATCAAGATGCTGACATCTATCTCTTGACATCATCTCTC	1501
QY	563	Ser Ala Val Asp Ala Gly Val Ser Arg His Leu Phe Glu Leu Cys Ile Cys Gln Ile Leu	582
Db	1502	AGTGNNNNNNNNNGCCGAAGTTAGCAGACACTTGTTCGAATCTGTATTTGTTCAAACTTTG	1561
QY	583	His Gly Lys Ile Thr Ile Val Val Thr His Gln Leu Gln Trp Leu Lys Ala Ala Ser Gln	602

Dd		1562	CATGGAAGATCACAAATTTTAAGTACCTCATCGATTGCATGTAACCTCAAGCTGCAGAATCAG	1621
Oy	IleuIleuIleuLyAspGlyLysMetValGlnLysGlyThrTrpArgLysPheLeuLys	603		622
Dd	ATTTCGATATTGGAAAAGATNGTMAAATGTGTGCAGAAAGGGAGCTTACACTGAAGTCTTAAAA	1602		1681
Oy	SerGlyIleasPheGlySerLeuLeuLysIleAspAsnGluSerGluGlnProPro	623		642
Dd	TCTGGTATAGATTTTGGCTCCCTTTTAAAGAGACAAACGGAAATGTAAACAACCTCCA	1682		1741
Oy	ValProGlyThrProThrLeuAspAsnArgPheSerGluSerSerValIleProSerGln	663		662
Dd	GTTCCAGGAACCTCCACACTGAGGAATGTGATCCTTCCAGAGCTTGTTGGTTGCTTCCAA	1742		1801
Oy	GlnSerSerArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlnLysVal	663		682
Dd	CAATTTCTTAACCTCCTCTTGAAGAGATGTGCTCTGAGAGCCCAAGTACAGAAATGTC	1802		1861
Oy	ProValThrLeuSerGluGlnLysAsnArgSerGluLysValGlyPheGlnAlaTyrlLys	663		702
Dd	CCAGTTACACTATCAGAGAGAAACCGTTCTGAAAGAAAGTAGTGGTTTTCAGGCTTAAG	1862		1921
Oy	AsnTyrrPheAspAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeuAsnThr	703		722
Dd	AATTACTTCAGAGGTGGTGCTCAGCTGGAATGTCTTCATTTTCTTATTTCTTCATAACACT	1922		1981
Oy	AlaAlaGlnValAlaTyrrValLeuGlnAspTrpTrpLeuSerTyrrTrpAlaAsnLysGln	723		742
Dd	GCAGCTCAGGTGGCTATGTCTTCAAGATTTGGTGGCTTTCATCTCGGCCAACAAACA	1982		2041
Oy	SerMetLeuAsnValIthrValAsnGlyGlyValAsnValThrglLysLeuAspLeuAsn	743		762
Dd	AGTATGCTAAATGTCACTGTAAATGAGAGAGAAATGAAACCGAAGACTAGATCTTAAC	2042		2101
Oy	TrpTyrrLeuGlyIleTyrrSerGlyLeuThrValAlaIthrValLeuPheGlyIleAlaArg	763		782
Dd	TGGATCTTAGGAATTTTATTCAGGTTTTAAACGTATCACTCCGTTCTTTCGCAATAGCAAGA	2102		2161
Oy	SerLeuLeuValPheTyrrValLeuValAsnSerSerGlnThrLeuHisAsnLysMetPhe	783		802
Dd	TCTCTATTGGTATTCATAGCTCTTGTATTACTTTCACAAACCTTGGCAACAATAATGTTT	2162		2221
Oy	GluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArgIleLeu	803		822
Dd	GAGTCAATTCGGAAGCTCGGATTTATTTCTTGATGAATCAATAGGAAGAAATTTTA	2222		2281
Oy	AsnArgPheSerLybAspIleGlyHisLeuAspAspLeuProLeuThrPheLeuAsp	823		842
Dd	AATGCTTCTCCAAAGACATTTGACACATCGATGATTTGCTGCGCTGACAGCTTTTATGAT	2282		2341
Oy	PheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaValIlePro	843		862
Dd	TTCAATCCANNNTTGTCAACAAGTGTGGTGTGTCTCTGTGGTGTGGCCGGATGATCTT	2342		2401
Oy	TrpIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArgTyrrPhe	863		882
Dd	TGGATCGGAATACCCTTGTTCCCTCCCTTGGAATCATTTTCTTGCGGCGAATATTTT	2402		2461
Oy	LeuGluThrSerArgAspValLysArgLeuGluSerThrThrArgSerProValPheSer	883		902
Dd	TTGGAAACGTCAAGATGTGAAGCGCTCGAATCTTCAACCTCGGAGTCCAGTGGTTTTCC	2462		2521
Oy	HisLeuSerSerSerLeuGlnGlyLeuLeuTrpThrIleArgAlaTyrrLysAlaGluGluArg	903		922
Dd	CACCTATCATTTTCTTCCAGGGGCTTGACCAATCCGGGCAATCAAAGCAAGAAAGAGG	2522		2581
Oy	CysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGlnLysAlaTrpPheLeuPheLeu	923		942
Dd	TGTGAGGAGACGTGTGATGACACACAGGAATTTACATTCAGAGGCTTGCTTGTTTTTG	2582		2641
Oy	ThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheValIleIle	943		962

Db 2642 ACAAGCTCCGCTGCTGCTGCTGCTGATGCCATCTGTCATGTTTGTCAATCATC 2701

Qy 963 ValAlaPheGlySerLeuIleLeuAlaValThrLeuAspAlaGlyValValGlyLeuAla 982

Db 2702 GTTGCCTTTGGTCCCTGATTTCTGGCAAAAACCTGGATGCCGGGAGGTTGGTTGGCA 2761

Qy 983 LeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTyrCysValArgGlnSerAlaGlu 1002

Db 2762 CTGCTCATGCGCTCACGCTCATCGGGGAGTGTTCAGTGGTGTGTTGCAAAAGTCCGCA 2821

Qy 1003 ValGlyAspMetMetIleSerValGlyValGlyValIleGluTyrThrAspLeuIlysglu 1022

Db 2822 GTTGGAAATATATGATCTCAGTAGAAAGGTCATTGAATACACAGACTTAAAAAGGA 2881

Qy 1023 AlaProTyrGlyTyrGlyIlyValArgPropProAlaTyrProHisGlyGlyValIleIle 1042

Db 2882 GCACTTGGGAATATCAGAAAGCCCAACCGGCTGGCCCTGAGAGAGATGATATAC 2941

Qy 1043 PheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValIleuIlyshisLeuThr 1062

Db 2942 TTTCACAATGTGAATCTCATGTACAGTCCAGGTGGGCTCTGGTACTGAAAGCATCTGACA 3001

Qy 1063 AlaLeuIleValSerGlnGlyValGlyIleValGlyArgThrGlyAlaGlyLysSer 1082

Db 3002 GCACTCATTAATCAACANN 3061

Qy 1083 SerLeuIleSerAlaLeuPheArgLeuSerGluProGlyGlyIlyIleTyrIleAspLys 1102

Db 3062 NNN 3121

Qy 1103 IleLeuThrThrGlyIleGlyLeuHisAspLeuArgLysLysMetSerIleIleProGln 1122

Db 3122 NNN 3181

Qy 1123 GluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlyHisThr 1142

Db 3182 GAACCTGTTTGTCTCATCGAAACAATGAGAAAAAACCTGATCTCTTATATAGCACAG 3241

Qy 1143 AspGlyGlyLeuTyrAsnAlaLeuGlnGlyValGlnLeuIlyGlyIleGlnAspLeu 1162

Db 3242 GATGAGAACTGTGGAATCCCTTACAGAGGTACCACTTAAAGAAACCTTGAAGTCTT 3301

Qy 1163 ProGlyLysMetCaspThrGlyLeuAlaGlySerGlySerAsnPheSerValGlyIlyArg 1182

Db 3302 CCTGTAAATGATGATCTGAATTAGACAGATCAGATTCATTTATGTGTGACAAAGA 3361

Qy 1183 GlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIleAspGlu 1202

Db 3362 CAACGTGTGTGCTTGCAGGGCAATCTCAGGAAAAATCAGATATGTATGATGAA 3421

Qy 1203 AlaThrAlaAsnValAspProArgThrAspGlyLeuIleGlnLysIleArgGlyLys 1222

Db 3422 GCGACGGCAATGTGATCCAGANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 3481

Qy 1223 PheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAspSerAsp 1242

Db 3482 NNN 3541

Qy 1243 LysIleMetValLeuAspSerGlyArgLeuLysGlyTyrAspGluProTyrValLeuLeu 1262

Db 3542 NNN 3601

Qy 1263 GlnAsnLysGlySerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGluAla 1282

Db 3602 CAAATTAAGAGAGCCTATTTTACAGAGTGTGCAACCACTGGGCAAGCAGCAAGCCGT 3661

Qy 1283 AlaLeuThrGlyThrAlaLysGln 1290

Db 3662 GCCCTACAGAAACAGCAAAACAG 3685

RESULT 5

AK032802

LOCUS AK032802 3208 bp mRNA linear HTC 03-APR-2004

DEFINITION Mus musculus 12 days embryo male wolffian duct includes surrounding region cDNA, RIKEN full-length enriched library, clone:6720455A17

ACCESSION AK032802.1 GI:26083045

VERSION AK032802.1

KEYWORDS HTc; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

PUBMED 11042159

AUTHORS Shbata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitanaka, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasahara, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Okazaki, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuda, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

TITLE RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

PUBMED 11076861

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)

JOURNAL Nature 420, 563-573 (2002)

AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arawaka, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kuribara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, K., Ohno, M., Ohsue, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shbata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.  
URL: <http://genome.gsc.riken.jp/>  
URL: <http://fantom.gsc.riken.jp/>.

## FEATURES

**Source**

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/dev_age="12 days embryo"
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/note="ATP-binding cassette, sub-family C (CFTR/MRP), member 4 homolog (Human) (SWISSPROT|O15439, evidence: FASTA, 86.9%ID, 98.1%length, match=3904)"

```

## ORIGIN

[illegible]

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Qy	817	ProIleGlyArgIleLeuAsnArgPheSerLysAspIleGlyHisIleuAspArgLeuLeu	833
Db	122	CCAAATGGAGAGATTTTAATCGTCTTCCAAAGACATGGACACATGATGATTTGCTT	181
Qy	837	ProLeuThrPheLeuAspPheIleGlnThrLeuGlnValAlaGlyValLysArgVal	856
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Qy	857	AlaValAlaValIleProThrIleAlaIleProLysValProLeuGlyIleIlePheIle	876
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Qy	877	PheLeuArgArgLysPheLeuGlnThrSerArgAspArgValLysArgLeuGluSerThr	896
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Db	782	CACAGAGGAGTCATCTCTTCGACAAATGTAACTTCACTACAGTTAGATGAGGCTCTG	841
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Qy	1137	ProPheAsnGluHsttHrAspGlnGluLeuTtPAsnAlaLeuGlnGluValGlnLeuYs	1156
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Qy	1197	IleLeuIleIleAspGluIatThrAlaAsnValAspProArgtHrAspGluLeuIleGln	1216
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DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4931419N09 product:ATP-binding cassette, sub-family C (CFTR/MRP), member 1a, full insert sequence.	AK029676.1	GI:26325799	HTC; CAP trapper.	Mus musculus (house mouse)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)	103496636				
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)	11042159				
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Katsuna, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)	11076861				
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)	5				
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)	6 (bases 1 to 5920)				
Fukuda, S., Aizawa, K., Akimura, T., Arkawa, T., Bono, H., Carninci, P., Akashi, S., Furuno, M., Hasegaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiroaka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Konda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shikawa, A., Shiraki, T., Sogabe, Y., Tegami, M., Tagawa, A., Takanaishi, F., Takaku-Akahira, S., Tanaka, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.					
Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Kanagawa 230-0045, Japan (E-mail: genome-resgsc@riken.jp, URL: http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)					
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.					
Please visit our web site for further details.					

[illegible]

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 Db 2983 -----CATGATCTGCAGCTGGCTTACCTATGGCTGAGCTGACAGATGACCC 3036  
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 ACCESSION  
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 VERSION  
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 HTC.  
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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.  
 REFERENCE  
 1 (bases 1 to 5899)  
 Koehler, K., Beyer, A., Mewes, H. W., Weil, B., Amid, C., Oanger, A.,  
 Fobo, G., Han, M. and Wiemann, S.  
 The German CDNA Consortium  
 Direct Submission  
 Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr. 1, D-85764  
 Neuherberg, GERMANY  
 COMMENT  
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
 Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;  
 Sequenced by BMFZ (Biomedical Research Center at the  
 Heinrich-Heine-University, Duesseeldorf/Germany) within the CDNA  
 sequencing consortium of the German Genome Project. This clone  
 (DKFZp781G125) is available at the RZPD Deutsches Ressourcenzentrum  
 fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD  
 for ordering:  
 http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp781G125  
 Further information about the clone and the sequencing project is  
 available at http://mips.gsf.de/projects/cdna/.  
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## ORIGIN

## Alignment Scores:

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Score: 2216.50
Percent Similarity: 56.3%
Best Local Similarity: 37.4%
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DB: 4
Gaps: 30

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US-09-976-858-42 (1-1325) x CR749835 (1-5899)

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QY 77 -----LysProSerLeuThr 81
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RESULT 8
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DEFINITION Mus musculus ATP-binding cassette, sub-family C (CFTR/MRP), member
ACCESSION BC046560
VERSION BC046560.1 GI:28279835
KEYWORDS HTC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 4547)
Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Scheiner, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Datchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stephenson, M., Soares, M.B., Bonaldi, M.F., Casavant, T.L.,
Scheer, T.E., Brownstein, M.J., Uedeli, T.B., Toshiyuki, S.,
Abramson, R.D., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
McWhirter, R.J., Malek, J.A., Gunaratne, P.H., McSwan, P.J.,
Wolfe, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Vallat, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahney, J., Hellon, E., Kertman, M., Madan, A., Young, A.C., Shcherbakov, Y.,
Boiffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Schermer, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length

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JOURNAL human and mouse cDNA sequences
PROC. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
REFERENCES 2 (bases 1 to 4547)
AUTHORS Straussberg, R.
TITLE Direct Submission
JOURNAL Submitted (04-FEB-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.ncl.nih.gov
REMARK Contact: MGC help desk
COMMENT Email: cga@bbs.fda.nih.gov
Tissue procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louised, H.,
Kowls, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nantavati,
A.N., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/BLM at: http://image.llnl.gov
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REFERENCE
1 (bases 1 to 4953)
Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,
Wong, G. K. S., Deng, X. W. and Wang, J.
An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
Unpublished (2004)
JOURNAL
COMMENT
Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
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Qy	573	Leu-----	573		
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 Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,  
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 White, T.J., Sniinsky, J.J., Adams, M.T.D. and Cargill, M.

TITLE A scan for positively selected genes in the Genomes of Humans and Chimpanzees  
 JOURNAL (er) Plos Biol. 3 (6), E170 (2005)  
 PUBMED 15869325  
 REFERENCE 2 (bases 1 to 4638)  
 AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civejlo,D., White,T.J., Sniinsky,J.J., Adams,M.D. and Cargill,M.  
 TITLE Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.  
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 1156 LysGluThrIleGluAspLeuProGlyLysMetAspThrGluLeuAlaGluSerGlySer 1175  
 4246 AAGCTTTTGTGGCAGGCTGCACTGGGTTATCTCCAGAAATGACAGAGGCTGTGGC 4305  
 1176 AsnPheSerValGlyGlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsn 1195  
 4306 AACCTGACATAGGCAAGAGAGCTGTGTGGCTGGCAGAGGCTCTGCTGGAATATCC 4365  
 1196 GlnIleLeuIleIleAspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIle 1215  
 4366 AAGATCTGTGCTGAGAGAGCCACTGCTCGGTGATCTTAGACAGACAACTCTATTT 4425  
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Db      4426 CAGACGACCATCAAAACAGATTGCGCCACAGTATCAACATCGCCACAGGCTG 4485
Qy      1226 AanthrilleAserSeraplysiMetValleuAserGlyArgleuylgIuYr 1255
Db      4486 CACACCATCATGACGATGACAGGTAATGTCCTAGACAGGAGATTATAGAGTGC 4545
Qy      1256 AepgluProTyValleuLeuGlnsAnlysgIuSerleuPheTyrlYseMetValgIngn 1275
Db      4546 GGCAGCGCTCGAAGAACTGCTACAA--ATCCCTGAGACCTTTTATGCTTAAGCTAGAA 4602
Qy      1276 LeuGly 1277
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LOCUS   DQ038460          4080 bp    DNA        linear    GSS 02-JUN-2005
DEFINITION Homo sapiens ABC12 gene, VIRUAL TRANSCRIPT, partial sequence,
ACCESSION DQ038460
VERSION   DQ038460.1 GI:66889669
KEYWORDS  GSS.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 4080)
AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B.,
          Whitez,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civeello,D.,
          Hubisz,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
          A Scan for Positively Selected Genes in the Genomes of Humans and
          Chimpanzees
JOURNAL   (er) PLOS Biol. 3 (6), E170 (2005)
PUBMED    15869325
REFERENCE 2 (bases 1 to 4080)
AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B.,
          Whitez,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civeello,D.,
          White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
          Direct Subnission
          Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
          Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering
          them based on alignment. Translation starts at the beginning of
          alignment.
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Percent:        2043.50      Matches:      479
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Best Local Similarity: 35.1%      Mismatches: 480
Query Match:    30.1%      Indels:      141
DB:             11          Gaps:      27

US-09-976-858-42 (1-1325) x DQ038460 (1-4080)
Qy      1 MetleuProVal-----TyrGlnGluValIysProAsnProleuGlnAspAlaAsnleu 18
Db      94 ATGATCCAGTCGACCCCTGTGCAAGTTTAGACCAACCGGTGATGATGCGGCGCTA 153
Qy      19 CysSerArgValPhePheTrpTrpLeuAsnProleuPheLysIleGlyHisIysArgGly 38

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Db      154 CTTCCTTCGCGACATTTTCTGCTCAGCCCGGTGATGTGMAAGCTTACCGGCAAG 213
Qy      39 LeuGlnGluAraPseMetTySerValleuProGluAraPseGlnHisleuGlylu 58
Db      214 CTGACCGTGAACACCCCTCCCAATTCGACATATGATGATCTGACACCAATGCCAA 273
Qy      59 GluLeuGlnGlyPheTrpAspLysGluValleuArgAlaGluAsnAspAlaGlnLysPro 78
Db      274 AGATTTCAGATCCTTTGGATGAAGAAGGTACCAAGGGTGG-----GGTCTGAGAAGGCC 327
Qy      79 SerleuThrArgAlaIleIleLysCysTyTrpLysSerTy----- 92
Db      328 TCTCTGACCAACGTGTG-----TGAAATTCGACAGACACGCGTGTGATG 375
Qy      93 --LeuValleuGlyIlePheThrleuIleGlnIuSerAlaLysValIleGlnProIle 111
Db      376 GACATCGTGGCCAAATCTGTGATGATATC-----ATGGACGATAGGGCGGTGAT 429
Qy      112 PheLeuGlyLysIleIleAsnTyPheGluAsnTyPheGluAsnTyPheMetAspSerValAlaLeu 131
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Qy      132 AanthralaTyAla--TyrAlaPheValleuThr-----PheCysThrleuIle 147
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Qy      148 LeuAlaIleLeuHisleuLeuTyPheTyHisValGlnCysAlaGlyMetArgLeuArg 167
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Qy      168 ValAlaMetCysHisMetIleTyArgLysAlaLeuArgLeuSerAsnMetAlaMetLys 187
Db      586 GTGGGCGCTCCACCTTGTTT-----GAAACCTGTGTCCTTC 627
Qy      188 LysThrThrThr-----GlyGlnIleValAsnLeuLeuSerAspValAsn 203
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Qy      204 LysPheAspGlnValThrValPheLeuHisPheLeuThrAlaGlyProleuGlnAlaIle 223
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Qy      264 LysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIleThrGlyIle 283
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Qy      284 ArgIleIleLysMetTyAlaTrpGluLysSerPheSerAsnLeuIleThrAsnLeuArg 303
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Qy      304 LysLysGluLysLeuIleLeuArgSerSerLysAsnGlyMetAsnLeuLysSer 323
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Qy      324 PhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyValleuLeuGly 343
Db      1048 GCGCCCATCGTGTCCACATAGCATCGGTGATATATCTGTGCACATCTCTCTGAGA 1107
Qy      344 SerValIleThrAlaSerArgValPheValAlaValThrLeuTyGlyAlaValArgLeu 363
Db      1108 CGCAAAATCAACGACCGCTGATTTAGTGTGATTTGCAATGTTAATGATATAGAGTT 1167
Qy      364 ThrValThrleuPhePheProSerAlaIleGluArgValSerGluAlaIleValSerIle 383
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Db      3322 GGGACCTGCTCCCAAGAC---TGGCCCACTGTGGGAGATGACCTTCAGAGACTATGAG 3378
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Db      3379 ATGAGATACAGACACACACCCCTGTGTTCGACAGCTTGAACCTTGAACTACAAAGT 3438
Qy      1068 GlnGluYsValGlyIleValGlyYrThrGlyAlaGlyYsSerSerLeuIleSerAla 1087
Db      3439 GGGCAGACAGTCCGAGATTTTGGAGAGACAGCTTCGGAAATCATCTGTAGAGATGCT 3498
Qy      1088 LeuPheArgLeuSerGluPro--GluGlyYsIleTPrIleAspIleLeuThrThr 1106
Db      3499 TTGTTTCGTCTGTGGAGACCACTGACAGTGGCACAACTTATGATGAGGTGATATCTGC 3558
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Qy      1127 PheThrGlyThrMetArgYsAsnLeuAspProPheAsnGlnHisThrAspGluGluLeu 1146
Db      3619 TTTGTAGGTACAGTAAAGTACAACTTGATCCCTTGAGAGTACACAGTATGAGATGCTC 3678
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LOCUS     Homo sapiens ABC5 gene, VIRUTAL TRANSCRIPT, partial sequence,
DEFINITION
ACCESSION AY407265
VERSION    AY407265.1 GI:39763236
KEYWORDS   GSS.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 4185)
AUTHORS   Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
          Todd,M.A., Tanenbaum,D.M., Civeillo,D.R., Lu,F., Murphy,B.,
          Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sniinsky,J.J.,
          Adams,M.D. and Cargill,M.
          Inferring nonneutral evolution from human-chimp-mouse orthologous
          gene titos
          JOURNAL
          Science 302 (5652), 1960-1963 (2003)
          PUBMED
          14671302

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REFERENCE 2 (bases 1 to 4185)
AUTHORS   Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
          Todd,M.A., Tanenbaum,D.M., Civeillo,D.R., Lu,F., Murphy,B.,
          Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sniinsky,J.J.,
          Adams,M.D. and Cargill,M.
          Direct Submission
          Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
          Rockville, MD 20850, USA
          This sequence was made by sequencing genomic exons and ordering
          them based on alignment.
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Qy      50 GlnAspArgSerGlnHisLeuGlyGlnGluLeuGlnGlyPheTrpAspYsGluValLeu 69
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Qy      70 ArgAlaGlnAspAlaGlnIleYsProSerLeuThrArgAlaIleIleYsCysTrp 89
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Qy      90 LysSerYrLeuValLeuGlyIlePheThrLeu---IleGlnGluSerAlaValIle 108
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Qy      109 GlnProIlePheLeuGlyYs---IleIleAsnYrPheGlnAsnYrAspProMetAsp 127
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Qy      128 SerValAlaLeuAsnThrAlaTrAlaTrAlaThrValLeuThrPheCysThrIleuIle 147
Db      499 -----GCAACAGACTTAACCTGACAGTACAGCTTGTGTGTGTGTGTGTGTGTGTGTGT 552
Qy      148 -----LeuAlaIleLeuHisLeuThrPheLeuThrPheLeuThrPheLeuThrPhe 159
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Qy      180 ArgLeuSerAsnMetAlaMetCylYsThrThrThrGlyGlnIleValAsnLeuLeuSer 199
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Qy      200 AsnAspValaAsnYsPheAspGlnValThrValPheLeuHisPheLeuThrAlaGlyPro 219
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 QY 240 GlyMetAlaValIleIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSer 259  
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 QY 417 AlaPheTrpAspLys----- 421  
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 QY 426 Pro----- 426  
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QY 507 ValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeuGluIleAspLeuThr 526  
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Qy      1067  SerGlnGluLysValGlyIleValGlyArgThrGlyAlaGlyLysSerSerleuLeu 1086
Db      3526 CCTAAAGAGAAATTTGGCATTTGGGGGCGGACAGATCAAGGAAGTCCGCTGGGGAG 3585
Qy      1087  AlaLeuPheArgLeuSerGluProGluGlyLys---IleTrpIleAspLysIleLeuThr 1105
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Qy      1106  ThrGlnIleGlyLeuHisAspLeuArgLysLysMetSerIleleProGlnIleProVal 1125
Db      3646 AGTGATATTGGCTTCCGACCTCCGAGACAACTCTTATATCATCTCTCAAGAGCGGGTG 3705
Qy      1126  LeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGluHisThrsAspGlu 1145
Db      3706 CTGTTACAGTGGCAGCTGTGATCAATTTGAACCCCTTCAACAGATCACTGAAGCCAG 3765
Qy      1146  LeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGluAspLeuProGlyLys 1165
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Db      3826 CTTGAATCTGAAGTGTGAGATGGGAGTAACCTTCTGATGGGAGAGCGAGCTCTTG 3885
Qy      1186  CysLeuAlaArgAlaIleleuArgLysAsnGlnIleleuIleleAspGluAlaThrAla 1205
Db      3886 TGCATATGTAGAGCCCTGCTCGGCACTGTAAAGATTCTGATTTTAAATGAAGCACAGCT 3945
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Db      3946 GCCATGACACAGAGACAGACTTATTGATTCAGAGACCATCCGAGAAACATTGGCAGAC 4005
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Db      4006 TGTACATGCTGACCATTCCTCCCATCGCTTCGACACAGGTTTCAGGCTCGATAGATTATG 4065
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Db      4066 GTGCTGGCCGACGAGCAGATGTGTGAGATTGACACCCATCGGTCTCTGTCCAAACGAC 4125
Qy      1266  GluSerLeuPheTrpLysMet 1272
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RESULT 13
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LOCUS Mus musculus ABC5 gene, VIRUTAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY407267
VERSION AY407267.1 GI:39763238
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 4176)
Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
location/Qualifiers
source
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ORIGIN
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Best Local Similarity: 34.4% Mismatches: 522
Query Match: 28.8% Indels: 137
Gaps: 26
DB: 10

US-09-976-858-42 (1-1325) x AY407267 (1-4176)
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Db      157  CACCAGTGGCAAAAGCTGAGACTTTCTCTACAGACACCTTTTCATGCTCTCTCTG 216
Qy      31  PheLysIleGlyHisLysArg---ArgLeuGluGluAspAspMetLysSerValLeuPro 49
Db      217  GCCCGAGTGTTCACAGAAAGGGGAGCTGTTAATGAGAGATGTGTGGCTTTGTCCAG 276

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Db	2356	CAGGTG-----GAGGAGAAAGGCGAAGGTTCTGTGTCCTTGCTGCTACGTACTCGG	2403
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Db	2404	GTCTACATCCAGGCGTGCAGGGGGGCCCTTGGGCTTTCCTGGATCATGATGTCCTCTCATG	2463
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Db	2464	CTGAATGTGGCAGCAGCTGCTTCAGCAGCTGTGGCTTACGTACTGATGC---AMGCA	2520
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Qy	761	-----LeuAsnTrrTyrLeuGlnIleTyrSerGlyLeuThrValAlaIleThrVal	776
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Qy	777	LeuPheGlyIleAlaArgSerIleuValPheTyrValIleuValAsnSerSerGlnThr	796
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Qy	797	LeuHisAsnIleMetPheGluSerIleLeuIleValAlaProValIleuPheAspArgAsn	816
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Qy	817	ProIleGlyArgIleLeuAsnArgPheSerIleAspIleGlnIleLeuAspIleu	836
Db	2761	CCAAAGAGAGGATTTCTACAGGTTTCCAAAGCAGATGAAAGTGGATGTGGCGCTG	2820
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Qy	897	ArgSerProValPheSerHisIleuSerSerIleuGlnIleTrrTrrIleArgAla	916
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Oy	1230	ThrIleAlaHisArgLeuAsnThrIleLleAspSerAspLysIleMetValLeuAspSer	1249
Db	4009	ACCAATTGCCATCGCTGCACACAGTCTCTGAGGACTCTGACAGATCAGTGTGCTGCCAG	4068
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DEFINITION OsBRM001445 Oryza sativa Expressed Sequence Tag (EST) cDNA			
ACCESSION CL957124			
VERSION CL957124.1 GI:52369499			
KEYWORDS GSS.			
SOURCE Oryza sativa (indica cultivar-group)			
ORGANISM Oryza sativa (indica cultivar-group)			
REFERENCE 1 (bases 1 to 4483)			
AUTHORS Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,			
Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,			
Wong, G. K. S., Deng, X. W. and Wang, J.			
TITLE An analysis of transcriptional regulation of the rice genome and			
JOURNAL its comparison to Arabidopsis			
COMMENT Unpublished (2004)			
Contact: Chen Chen			
Department of Bioinformatic			
Beijing Institute of Genomics			

Chinese Academy of Sciences, Beijing 101300, China

Tel: 86-10-80481559  
Fax: 86-10-80488676

Email: chenchen@genomics.org.cn

Rice genomic sequence.

Class: exon-trapped.

FEATURES  
source location/Qualifiers

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# ORIGIN

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Pred. No.: 1.01e-206 Length: 4483  
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Percent Similarity: 54.84 Conservative: 263  
Best Local Similarity: 34.48 Mismatches: 524  
Query Match: 28.84 Indels: 57  
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US-09-976-858-42 (1-1325) x CL957124 (1-4483)

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Db 925 GTCCGGGTGACCGCTTCACGCTGTGCTACACAGCTTCACCTACGTGCGCTTAC 984  
Oy 112 PheLeuGlyLysIleIleAsnTyrPheGluAenTyrAspProMetAspSerValAlaLeu 131  
Db 985 CTCATCGACGCTGCTGCAATAC-----CTC 1011  
Oy 132 AenThrAlaTyrAlaTyrAlaThr-----ValLeuThrPheCysThrLeuIleLeu 148  
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RESULT 15  
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 LOCUS CL970490  
 DEFINITION OsiRCC019970 Oryza sativa Exprese linear Oryza sativa (indica  
 cultivar-group) genomic, genomic survey sequence.  
 ACCESSION CL970490  
 VERSION CL970490.1 GI:52395588





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 Db 2485 CTCTGTCATCCGGCAGCGCATTTCCAGACAGCTTGTG-----AATCGCAACAAGAC 2535  
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Job time : 11411 secs

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GenCore version 5.1.7  
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## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 14, 2006, 09:29:33 ; Search time 515 Seconds

(without alignments)  
4573.338 Million cell updates/sec

Title: US-09-976-858-42

Perfect score: 6767  
Sequence: 1 MLPYQVEKRPDLQANLCS.....MTNTNSQNPSTLTFETAL 1325

## Scoring table:

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

## Command line parameters:

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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2	6760	99.6	6082	3	US-09-439-313-535
3	6760	99.6	6082	3	US-09-636-215-535
4	6760	99.6	6082	3	US-09-685-166A-535
5	6760	99.6	6082	3	US-09-679-426-535
6	6760	99.6	6082	3	US-09-759-143-535
7	6760	99.6	6082	3	US-09-651-236-535
8	6760	99.6	6082	3	US-09-657-279-535
9	6760	99.6	6082	3	US-10-012-896-535

10	6600.5	97.3	6140	3	US-09-439-313-536	Sequence 536, App
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14	6600.5	97.3	6140	3	US-09-759-143-536	Sequence 536, App
15	6600.5	97.3	6140	3	US-09-651-236-536	Sequence 536, App
16	6600.5	97.3	6140	3	US-09-657-279-536	Sequence 536, App
17	6600.5	97.3	6140	3	US-10-012-896-536	Sequence 536, App
18	6357	93.7	4395	3	US-10-012-896-1007	Sequence 1007, App
19	6354	93.6	3786	3	US-10-012-896-1006	Sequence 1006, App
20	2298.5	33.9	5011	2	US-08-141-893-1	Sequence 1, App1
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38	2145	31.6	5232	3	US-08-972-927-1	Sequence 1, App1
39	2123	31.3	5079	3	US-09-647-140B-5	Sequence 5, App1
40	2111	31.1	5175	3	US-08-972-927-4	Sequence 4, App1
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## ALIGNMENTS

RESULT 1  
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; Sequence 1, Application US/09647140B  
; Patent No. 6803184  
; GENERAL INFORMATION:  
; APPLICANT: Fox Chase Cancer Center  
; APPLICANT: Krub, Gary D.  
; APPLICANT: Lee, Kun  
; APPLICANT: Belinsky, Martin G.  
; APPLICANT: Bain, Lisa J.  
; TITLE OF INVENTION: MRP-Related ABC Transporter Encoding  
; TITLE OF INVENTION: Nucleic Acids and Methods of Use Thereof  
; FILE REFERENCE: FCCC 98-02  
; CURRENT APPLICATION NUMBER: US/09/647,140B  
; CURRENT FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: PCT/US99/06644  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 60/079,759  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/095,153  
; PRIOR FILING DATE: 1998-08-03  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 4231  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-647-140B-1  
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Pred. No.: 0  
Score: 6779.00  
Percent Similarity: 99.94  
Length: 4231  
Matches: 1323  
Conservative: 1

Best Local Similarity: 99.8% Mismatches: 1  
Query Match: 99.9% Indels: 0  
DB: 3 Gaps: 0  
US-09-976-858-42 (1-1325) x US-09-647-140B-1 (1-4231)

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QY 441 LeuAlaValIleGlyProValIleGlyLysSerSerLeuLeuSerAlaValLeuGly 460  
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QY 461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTrpValSerGln 480  
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 QY 741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyValAsnValThrGlnLysLeuAsp 760  
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 Db 2396 CTTAATCTGACTTGAATTTATTCAGGTTTAACTGTAAGCTTCTTCTTCTTCTTCTTCTTCTT 2455  
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Db 3296 CTGACAGACACTTAATTAATCAAGAAAGGTTGGCATTTGGGAAGAACCGGAGCTGGA 3355  
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RESULT 2  
 US-09-439-313-535  
 ; Sequence 535, Application US/09439313  
 ; Patent No. 6329505  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Dillon, David C.  
 ; APPLICANT: Mitchem, Jennifer L.  
 ; APPLICANT: Harlocker, Susan Louise  
 ; APPLICANT: Jiang Yuguang  
 ; APPLICANT: Reed, Steven G.  
 ; APPLICANT: Kalos, Michael  
 ; APPLICANT: Fanger, Gary  
 ; APPLICANT: Retter, Mark  
 ; APPLICANT: Solk, John  
 ; APPLICANT: Day, Craig  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER



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/ FILE REFERENCE: 210121.427C9
/ CURRENT APPLICATION NUMBER: US/09/439,313
/ CURRENT FILING DATE: 1999-11-12
/ NUMBER OF SEQ ID NOS: 575
/ SOFTWARE: FASTSEQ for Windows Version 3.0
/ SEQ ID NO: 535
/ LENGTH: 6082
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-439-313-535

Alignment Scores:
Pred. No.: 0          Length: 6082
Score: 6760.00       Matches: 1324
Percent Similarity: 99.9%    Conservative: 0
Best Local Similarity: 99.9%  Mismatches: 1
Query Match: 99.6%         Indels: 1
DB: 3                      Gaps: 0

US-09-976-858-42 (1-1325) x US-09-439-313-535 (1-6082)

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QY      41 GluAspAspMetTySerValLeuProGluAspArgSerGlnHisLeuGlyGluLeu 60
DB      306 GAAGATGATATGATATTCAGTGTGCGCAGAAAGCCGCTCACAGACCTTGAGAGGAGTTG 365
QY      61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAspAspAlaGlnLysProSerLeu 80
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QY      121 GluAsnTyAspProMetAspSerValAlaLeuAsnThrAlaTyAlaThrVal 140
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QY      201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
DB      786 GATGTGAACAAGTTGATCATCGTGACAGTGTCTTACATCTCTGTGGGCAAGACACACAG 845
QY      221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGlnIleGlyTyrLeuSerCysLeuAlaGly 240
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QY      241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyTyrLeuPheSerSer 260
DB      906 ATGGAGTTCTATATCATCTCTCCCTGCAAAAGCTGTTTGGGAAGTTGTTCTATCA 965
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QY      561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGlnLeuLysIleCysGln 580
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QY      581 IleLeuHisGlyLysIleThrIleLeuValThrHisGlnLeuGlnTyPheLysAlaIle 600
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QY      601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyThrGlnPhe 620
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 Db 3726 CAAGACAACTGCTGTGCTTCCAGGCAATTTCTCAGAAACCAATATATATATATAT 3785  
 Qy 1201 AspGluAlaThrAlaAaAaValAaPProArgThrAaPGLuLeuIleGlnLysLysIleArg 1220  
 Db 3786 GATGAAGCAGCGCAATGTGATTCAGAACTGATGCTTATATCAAAAAAATC-CGG 3844  
 Qy 1221 GluLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAaAaThrIleIleAaP 1240  
 Db 3845 GAGAAATTTGCCCACTGACCGGTCTATACATTTGACACAGATTTGAACCATTTATGAC 3904  
 Qy 1241 SerAaPLeuIleMetValLeuAaPSerGlyArgLeuLysGluTyrAaPGLuProTyrVal 1260  
 Db 3905 AGCGACAAATATATGTTTATGATTCAGAGACACTGAAAGATATGATGAGCCGTATGT 3964  
 Qy 1261 LeuLeuGlnAaAaLysSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280  
 Db 3965 TTGCTGCAAAATTAAGAGAGCTTATTTACAGAGTGGTCAACCACTGGGACAGGACAG 4024  
 Qy 1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAaAaTyrProHisIle 1300  
 Db 4025 GCCGCTGCTCCTCACTGAACAGCAAAACAGATATCTTCAAAAGAAATTTATCCACAT 4084  
 Qy 1301 GlyHisThrAaPLeuMetValThrAaAaThrSerAaAaGlyGlnProSerThrLeuThrIle 1320  
 Db 4085 GGTCACTGACCACTATGTTTAAACCACTTCAATGACAGAGCCCTGACCTTATCATAT 4144  
 Qy 1321 PheGluThrAlaLeu 1325  
 Db 4145 TTCAGACAGCACTG 4159

RESULT 3  
 US-09-636-215-535  
 ; Sequence 535, Application US/09636215

Patent No. 6620922  
 GENERAL INFORMATION:  
 APPLICANT: Xu, Jiangchun  
 APPLICANT: Dillon, Davin C.  
 APPLICANT: Mitcham, Jennifer L.  
 APPLICANT: Harlocker, Susan L.  
 APPLICANT: Jiang, Yuqi  
 APPLICANT: Henderson, Robert A.  
 APPLICANT: Kalos, Michael D.  
 APPLICANT: Fanger, Gary R.  
 APPLICANT: Retter, Marc W.  
 APPLICANT: Stolk, John A.  
 APPLICANT: Day, Craig H.  
 APPLICANT: Vedrick, Thomas S.  
 APPLICANT: Vedrick, Derrick  
 APPLICANT: Li, Samuel  
 APPLICANT: Wang, Aijun  
 APPLICANT: Skeiky, Yasir A.W.  
 APPLICANT: Hepler, William  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 FILE REFERENCE: 210121.42717C17  
 TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
 CURRENT APPLICATION NUMBER: US/09/636,215  
 NUMBER OF SEQ ID NOS: 852  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 535  
 LENGTH: 6082  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-09-636-215-535

## Alignment Scores:

Pred. No.: 0 Length: 6082  
 Score: 6760.00 Matches: 1324  
 Percent Similarity: 99.9% Conservative: 0  
 Best Local Similarity: 99.9% Mismatches: 1  
 Query Match: 99.6% Indels: 0  
 DB: 3 Gaps: 0

US-09-976-858-42 (1-1325) x US-09-636-215-535 (1-6082)

QY 1 MetLeuProValTyrGlnGluValIysProAsnProLeuGlnAspAlaAsnLeuCySer 20  
 DB 186 ATGCTGCCCGTGTACAGAGAGGTGAAGCCCAACCCGCTGACAGACCGCAACCTTGCTCA 245  
 QY 21 ArgValPhePheTrpTrpLeuAsnProLeuPheIleGlyHisIleValArgGluGlu 40  
 DB 246 CCGGTGTTCTTCTGCGGTCAATCCCTGTAAATTGGCCATTAACGGAGATTAAAG 305  
 QY 41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGlnGluLeu 60  
 DB 306 GAAAGATGATATGATTCACTGCTGCCAAGACCGCTCACAGCACTTGGAGAGAGTTG 365  
 QY 61 GlnGlyPheTrpAspIysGluValLeuArgAlaGluAsnAspAlaGlnIysPheSerLeu 80  
 DB 366 CAAGGTTCTGGATTAAGAAGTTTAAAGCTGAAGATGACGACAGAAAGCTTCTTAA 425  
 QY 81 ThrArgAlaIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 100  
 DB 426 ACAAGGACATCATTAAGTTAACTGGAATCTTATTGTTTGGAAATTTTTCGTTA 485  
 QY 101 IleGlnGluSerAlaIleValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPhe 120  
 DB 486 ATTTGAGAAAGTGCACAAAGTAATCCAGCCATTTTGGAAAAATTTTAAATTTT 545  
 QY 121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaThrVal 140  
 DB 546 GAAATATTAGATCCCATGATTCGTGGCTTGAACACAGCCGATGACCGTACGCGT 605  
 QY 141 LeuThrPheCyThrLeuIleLeuAlaIleLeuHisIleLeuTyrPheTyrHisValGln 160  
 DB 606 CTGACTTTTGGACGCTCATTTTGGCTATACTGCATCACTTATATTTTATCACGTTG 665

QY 161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgIleAlaLeuArg 180  
 DB 666 TGTGCTGGATGAGGTTTACAGATGAGCATGTGCATATGATTATCGAAGGCACTTCGT 725  
 QY 181 LeuSerAsnMetAlaMetGlyLysThrThrGlyGlnIleValAsnLeuLeuSerAsn 200  
 DB 726 CTTAGTAAACATGCGCCATGGGAAGCAACACAGGCCGATGATGCAATCTCTGTCAT 785  
 QY 201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuThrAlaGlyProLeu 220  
 DB 786 GATGTAAACAGTTTGTATCAAGTGAAGTATCTTCACTTCTGTTGGGACAGACCACTG 845  
 QY 221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240  
 DB 846 CAGCGGATCGCATGACCTCCCTACTCGATGAGATGAGAAATTCGTGCTGCTGG 905  
 QY 241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260  
 DB 906 ATGGCAGTTCTAATCATTTCTCCCTGCGCAAGCTGTTTGGAAAGTTGTTTCATCA 965  
 QY 261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280  
 DB 966 CTGAGAGTAAACCTGCACCTTTCACGATGCCAGATCAGACCATGATGAAGTTTATA 1025  
 QY 281 ThrGlyIleArgIleIleIleIleMetTyrAlaTrpGluIysSerPheSerAsnLeuIleThr 300  
 DB 1026 ACTGTTATAGAGTATATAAATGTACCTCGGAAAAAGTCATTTTCAATCTTATATACC 1085  
 QY 301 AsnLeuArgLysGluIleSerLysIleLeuArgSerSerCysLeuArgIleMetAsn 320  
 DB 1086 AATTGAGAAAAAGAGAAATTTCCAAAGATTCGAGAAAGTTCTGCTCAAGGGAGAT 1145  
 QY 321 LeuIleSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340  
 DB 1146 TTGGCTTGTTTTCATGTCAGCAAAATCATCGTTTGTGACCTTACCACTTACCTG 1205  
 QY 341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360  
 DB 1206 CTCCTCGGAGTGTATCACAGCCAGCCGCGTTCGTCGAGTACCTGATGAGGCT 1265  
 QY 361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380  
 DB 1266 GTGCGCTGACGAGTATCCCTCTTCTTCCCTCAGCATTTGAGAGGTCACAGAGCAATC 1325  
 QY 381 ValSerIleArgArgIleGlnThrPheLeuLeuAspGluIleSerGlnArgAsnArg 400  
 DB 1326 GTACACATCCGAAGATCCAGACTTTTGTCTACTTGATGAGATTCACAGCGCAACCT 1385  
 QY 401 GlnLeuProSerAspGlyLysLeuMetValHisValGlnAspPheThrAlaPheTrpAsp 420  
 DB 1386 CAGCTGCCGTGACATGATTAAGATGATGATGATGATGATGATGATGATGATGATGAT 1445  
 QY 421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440  
 DB 1446 AAGGATGACAGACCCCACTTACAGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1505  
 QY 441 LeuAlaValIleGlyProValGlyValIleGlyLysSerSerLeuLeuSerAlaValLeuGly 460  
 DB 1506 TTAGCTGTGTGCGCCCGTGGAGACAGAGATCATCATCTTTAAGTGCCTGCTCGGG 1565  
 QY 461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaTyrValSerGln 480  
 DB 1566 GAATTTGGCCCAAGTCAAGGGGTGTGTCAGCGTCAAGTGAAGATTCCTATGTGCTCAG 1625  
 QY 481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrGlu 500  
 DB 1626 CAGCCCTGCGTGTCTCCGGAACCTCGAGAGTATATTTTATTTTGGAGAAAAATACAA 1685  
 QY 501 LysGluArgTyrGluLysValIleLysValAlaCysAlaLeuLysValAspLeuGlnLeuLeu 520  
 DB 1686 AAGGACATATGAAAAAGTCAATAAGGCTGTGCTGAAAAAGATTTTACAGCTGTG 1745

QY 521 GluAserGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnlys 540  
 Db 1746 GAGGATGGTGATCTGATCTGTGATAGAGATCCGGGAAACCACTGATGAGGAGGAGAA 1805  
 QY 541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560  
 Db 1806 GCACGGGTAAACCTTGCAAGACAGATGTATCAAGATGTCGATCATCTATCTCTGAGCAT 1865  
 QY 551 ProLeuSerAlaValAspAlaGlnValSerArgHisLeuPheGlnLeuGlyIleCysGln 580  
 Db 1866 CCTTCAGGAGAGTGAATGCGAAGTTCAGACACCTGTGTGAACCTGTGATTTGTCA 1925  
 QY 581 IleLeuHisGlnLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuLysAlaIle 600  
 Db 1926 ATTTTGATGAGAAAGATCAATTTTATGACTCATCTCACTGACGACTCAAGCTGCA 1985  
 QY 601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyTyrThrThrGlnPhe 620  
 Db 1986 AGTCAGATTCTGATATTGAAAGATGGTAAATGCTGACAAAGGGGACTTACACTGAGTTTC 2045  
 QY 621 LeuLysSerGlyIleLeuAspPheGlySerLeuLeuLysLysAspAsnGlnGlnSerGlnGln 640  
 Db 2046 CTAAATATCGTATGATATTGGCTCCCTTTAAAGAAAGATATGAGGAAAGTGAAACA 2105  
 QY 641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGlnSerSerValTyr 660  
 Db 2106 CCTCCAGTTCCAGAACTCCCACTAAGGAATCTGACTTCTCAGAGCTTCGGTTTGG 2165  
 QY 661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGlnSerGlnAspThrGln 680  
 Db 2166 TCTCAACAATCTTTAGACCTCTTGAAAGATGGTCTCTGAGAGCCAAATACAGAG 2225  
 QY 681 AsnValProValThrLeuSerGlnGlnAsnArgSerGlnGlyLysValGlyPheGlnAla 700  
 Db 2226 AATGTCACAGTACCTATCAGAGAGAACCGTTCTGAAGAAAGTGGTTTTCAGGCC 2285  
 QY 701 TyrLysAsnTyrPheArgAlaGlyAlaHisTyrIleValPheIlePheLeuIleLeuLeu 720  
 Db 2286 TTTAAGATTAATCTTCAAGCTGTGTCTCACTGATTTGTTCTTCAATTTTCTTCTCTA 2345  
 QY 721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTyrTyrLeuSerTyrTyrAlaAsn 740  
 Db 2346 AACACTGACGCTCAGGTGCTATGATGCTTCAAGATGGTGGCTTCAATACAGGCAAC 2405  
 QY 741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyValAsnValThrGlnLysLeuAsp 760  
 Db 2406 AAACAAGATGCTAAATGCTCACTGTAATGAGAGAGAAATGTAACCAAGAGCTAGAT 2465  
 QY 761 LeuAsnTyrTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780  
 Db 2466 CTTAACCTGATCTTGAATTTATTCAGGTTTAACTGATGCTAACCGTTCTTTTGGCAT 2525  
 QY 781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800  
 Db 2526 GCAAGATCTCTATGATGATTCACGCTGTTAACTCTTCAAAACCTTGCAACAACAA 2585  
 QY 801 MetPheGlnSerIleLeuLysAlaProValLeuPhePheAspArgAspProIleGlyArg 820  
 Db 2586 ATGTTTGATCAATCTGAAGCTCCGGTATTAATCTTTGATAGAAATCCAAATAGAGAGA 2645  
 QY 821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840  
 Db 2646 ATTTTAAATCGTTTCTCCAAAGACATGAGACCTTGAGATTTGTGCGCTGACGTTT 2705  
 QY 841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860  
 Db 2706 TTAAGATTCATCAAGCATTTGCTACAAAGTGGTGGTGTCTGCTGCTGCTGCGCGG 2765  
 QY 861 IleProTyrIleAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuArgArg 880  
 Db 2766 ATTCCTTGATGCAATACCTTGTGTTCCCTTGGATCATATTTTCTTCTGCGGCA 2825  
 QY 881 TyrPheLeuGlnThrSerArgAspValLysArgLeuGlnSerThrThrArgSerProVal 900

Db 2826 TATTTTGAAGACGTCAAGAGATGTGAAGCGCTCGAATCTACAACTCGGAGTCCAGTG 2885  
 QY 901 PheSerHisLeuSerSerSerLeuGlnGlyLeuTyrTyrIleArgAlaTyrLysAlaGln 920  
 Db 2886 TTTTCCCACTTGATATCTTCTCTCCAGGGGCTCTGAGACATCCGGGCTATCAACCAAGA 2945  
 QY 921 GluArgCysGlnGlnLeuPheAspAlaHisGlnAspLeuHisSerGlnAlaTyrPheLeu 940  
 Db 2946 GAGAGTTCAGAACTTTTATGATGACACCAAGATTTTACATTCAGAGGCTTGTCTTG 3005  
 QY 941 PheLeuThrThrSerArgTyrPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960  
 Db 3006 TTTTGAACAAGTCCCGCTGGTGGCGCTCCGCTGATGATGCATCTGAGCATGTTTTC 3065  
 QY 961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980  
 Db 3066 ATCATCGTTGCTTGGTGTCCCTGATTTCTGCAAAACTCTGAGATGCCGGGCGAGTTGGT 3125  
 QY 981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTyrCysValArgGlnSer 1000  
 Db 3126 TTGGCACTGCTTATGCTTCCCTCACTGAGGATGTTTCAAGTGTGTGTTGACAAAGT 3185  
 QY 1001 AlaGlnValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGln 1020  
 Db 3186 GCTGAAGTTGAGAAATATGATGATCTCAATGAAAGGTCATTTGAATACACAGACTTGA 3245  
 QY 1021 LysGlnAlaProTyrGlnTyrGlnLysArgProProValTyrProHisGlnGlyVal 1040  
 Db 3246 AAAGAAAGCACTTGGGAATATCAGAAACCCCAACCAAGCTGCCCCATGAAAGAGTG 3305  
 QY 1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060  
 Db 3306 ATTAATCTTGACAAATGTAATCTCACTGACAGTCCAGGTTGGCTCTGCTGATCAAGCT 3365  
 QY 1061 LeuThrAlaLeuIleLysSerGlnGlnLysValGlyIleValGlyArgThrValAlaGly 1080  
 Db 3366 CTGACAGACATCAATTAATACAAAGAAAGGTGGCATTTGGGAAAGAACGGAGCTGGA 3425  
 QY 1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGlnProGlnGlyLysIleTyrIle 1100  
 Db 3426 AAAAGTCCCTCATCTCCAGCCCTTTTGTAGTTGTTCAGAACCCGAAGGTAAATTTGGATT 3485  
 QY 1101 AspLysIleLeuThrThrGlnIleGlyLeuHisAspLeuArgLysMetSerIleIle 1120  
 Db 3486 GATTAAGATCTTGACAACTGAAATGACTTCAAGATTTAAGAAAGAAATGTCATCAT 3545  
 QY 1121 ProGlnGlnProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGln 1140  
 Db 3546 CCTCAGAACTGTTTCTTCTCACTGAAACATGAGAAACCTGATCCCTTTAATGAG 3605  
 QY 1141 HisThrAspGlnGlnLeuTyrAsnAlaLeuGlnGlnValGlnLeuLysGlnThrIleGln 1160  
 Db 3606 CACACGATGAGAACTGTGAATGCTTAAACAAGGTACAACTTAAAGAAACCAATTGA 3665  
 QY 1161 AspLeuProGlyLysMetAspThrGlnLeuAlaGlnSerGlySerAsnPheSerValGly 1180  
 Db 3666 GATCTTCTGTAATAATGATATCTGAATTAAGAGATACGAATCCAAATTTATGTTGGA 3725  
 QY 1181 GlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIle 1200  
 Db 3726 CAAGACAACTGTGTGCTGCTTCCAGGGCAATTCACAGAAATCAATATGATTTAT 3785  
 QY 1201 AspGlnAlaThrAlaAsnValAspProArgThrAspGlnLeuIleGlnLysLysIleArg 1220  
 Db 3786 GATGAAGGAGCGGCAATAGTGATCCAAAGACTGATGAGTTAATCAAAAAAATC-CGG 3844  
 QY 1221 GlnLysPheAlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAsp 1240  
 Db 3845 GAGAAATTTGCCCATGACCGGTGTAACATGACACAGATTTGAACCACTTATTAAC 3904  
 QY 1241 SerAspLysIleMetValLeuAspSerGlyArgLeuLysGlnTyrAspGlnProTyrVal 1260

Db 3905 AGCGACAAGATGATGTTTACAGGAGACTGAAAGAAATATGATGAGCCGTATGTT 3964  
QY 1261 LeuLeuGlnAsnLysGluSerLeuPheTyrLysMetValGlnGlnLeuGlyLysAlaGlu 1280  
Db 3965 TTGCTGCAGAAATTAAGAGAGCTTATTTTTCAGAGATGCTGCAACATCGGCGAGGACAGA 4024  
QY 1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300  
Db 4025 GCCGCTGCCCTCAGTGAACACGAAACAGGTATCTTCAAAAGAAATATTCACATATTT 4084  
QY 1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320  
Db 4085 GGTTCACACTGACCAATGGTATCAACACCTTCAATGAGACGCCCTGACCTTAATATT 4144  
QY 1321 PheGluThrAlaLeu 1325  
Db 4145 TTGAGACAGCACTG 4159  
RESULT 4  
US-09-685-166A-535  
; Sequence 535, Application US/09685166A  
; Patent No. 6630305  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, David C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuxi  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Reiter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William  
; APPLICANT: Hepler, William  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.427C21  
; CURRENT APPLICATION NUMBER: US/09/685,166A  
; CURRENT FILING DATE: 2000-10-10  
; NUMBER OF SEQ ID NOS: 898  
; SOFTWARE: FastSeq for windows Version 3.0  
; SEQ ID NO 535  
; LENGTH: 6082  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-685-166A-535  
Alignment Scores:  
Pred. No.: 0 Length: 6082  
Score: 6760.00 Matches: 1324  
Percent Similarity: 99.9% Conservative: 0  
Best Local Similarity: 99.9% Mismatches: 1  
Query Match: 99.6% Indels: 1  
DB: 3 Gaps: 0  
US-09-976-858-42 (1-1325) x US-09-685-166A-535 (1-6082)  
QY 1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20  
Db 186 ATGCTGCGGTGACCAAGAGGTGAAGCCCAACCGCTGAGAGCGGAACTTCTGCTCA 245  
QY 21 ArgValPhePheTyrTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlu 40  
Db 246 CGGTGTCTTCTGGTGGCTCAATCCCTTTTAAATTGGCCATTAACGGAATTAAGG 305  
QY 41 GlnAspAspMetTyrSerValLeuProGlnAspArgSerGlnHisLeuGlyGlnGluLeu 60

Db 306 GAAGATGATATGATATTCAGTCTGCGAGAGACCGCTCACAGCACCTTGAGAGAGGTGG 365  
QY 61 GlnGlyPheTyrAspLysGlnValLeuArgAlaGlnAsnAspAlaGlnLysProSerLeu 80  
Db 366 CAAGGTTCTCGAGATTAAGAAAGTTTAAAGACTGAGATGACGCAACAGACCTTCTTTA 425  
QY 81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100  
Db 426 ACNAGAGCAATCATTAAGATGTATCTGGAATCTTATTTAGTTTGGAAATTTTTCGTTA 485  
QY 101 IleGlnGluSerAlaLysValIleGlnProIlePheLeuGlyLysIleAsnTyrPhe 120  
Db 486 ATTAGAGAAAGTCCAAAGTATCCAGCCCATATTTTGGGAAATATTAATATATTTT 545  
QY 121 GlnAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrVal 140  
Db 546 GAAATTTATGATCCCATGATTCGTGTGCTTGAACAACAGGTCACGCTATGCGCAGTG 605  
QY 141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisIleLeuTyrPheTyrHisValGln 160  
Db 606 CTGACTTTTTCACGCTCATTTTGGCTATGCTGATTCATATTTTATTCACGTTGAG 665  
QY 161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180  
Db 666 TGTGCTGGAGATGAGTTACAGATGACCATGTGCCATATGATTTATTCGAGCACTTGT 725  
QY 181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuSerAsn 200  
Db 726 CTTAGTTAATGCGCATGGGAGAAACCAACACAGCCAGATGTCATCTGCTGCCAAT 785  
QY 201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuThrAlaGlyProLeu 220  
Db 786 GATGTGAACAAATTGATCATCGGTGACAGTTCCTTACACTTCTGTGGACAGACACTTG 845  
QY 221 GlnAlaIleAlaValThrAlaLeuLeuTyrMetGlnIleGlyIleSerCysLeuAlaGly 240  
Db 846 CAGGCGATCGACGTACATGCTTACTGTGAGAGAGATAGAAATCGGCTTCTGCGG 905  
QY 241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260  
Db 906 ATGGCAATTCATATCATTTCTGCTGCCCTTGCACAACTGTTTGGGAAAGTTGTCATCA 965  
QY 261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280  
Db 966 CTGAGAGATTAACCTGCACTTTCACAGATGCAAGATCAGGACCATGATATAAGTTATA 1025  
QY 281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300  
Db 1026 ACTGGTATAGATTAATTAATAATGTACGCTGGAAGAGTCAATTTCAAACTTATTAAC 1085  
QY 301 AsnLeuArgLysGlnLysSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320  
Db 1086 AATTTGAGAAACAGAGATTTTCCAAGATTCGAAAGTTCTGCTCCAGCGGAGTGAAT 1145  
QY 321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340  
Db 1146 TTGGCTCTCTTTTTCAGTGCAGCAAAATCATCGTGTGTGACCTTCCACCTACGCG 1205  
QY 341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360  
Db 1206 CTCTCTGGAGGTGTATCATCAGCCAGCCGCGTGTGTGGACGTACGTGATGGGGGT 1265  
QY 361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380  
Db 1266 GTGGCGCTACCGGTACCTCTTCTTCCCTCAGCACTGAGAGGGGTGCACAGCGCAATC 1325  
QY 381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluLysSerGlnArgAsnArg 400  
Db 1326 GTTCAGCATCCGAAGATCCAGACCTTTTGTCACTTGAAGAATACACAGCGCAACCGT 1385  
QY 401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTyrAsp 420  
Db 1386 CAGCTGCGGTCAAGATGGTAAAGATGTGATGTGACAGATTTTATCTCTTTTGGAT 1445

QY 421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440  
 DB 1446 AAGGATCATGAGAACCCCACTTACAGAGCCCTTCTTACTGTCTGAGACTGCGCAATTG 1505  
 QY 441 LeuAlaValAlaGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460  
 DB 1506 TTAGCTGTGTGCGCCCGCTGGAGAGAGGAGTCACTGTAAAGTCCGTGCTCGGG 1565  
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RESULT 5
US-09-679-426-535
Sequence 535, Application US/09679426
Patent No. 679515
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
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APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darwick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skelley, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C20
CURRENT APPLICATION NUMBER: US/09/679,426
CURRENT FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 895
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 535
LENGTH: 6082
TYPE: DNA
ORGANISM: Homo sapiens
US-09-679-426-535
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Score: 6760.00 Matches: 1324
Percent Similarity: 99.9% Conservative: 0
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Query Match: 99.6% Indels: 1
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/ APPLICANT: Stolk, John A.
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/ APPLICANT: Carter, Darrick
/ APPLICANT: Li, Samuel
/ APPLICANT: Wang, Aijun
/ APPLICANT: Skeiky, Yasir A.W.
/ APPLICANT: Hepner, William
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
/ FILE REFERENCE: 210121.427C23
/ CURRENT APPLICATION NUMBER: US/09/759,143
/ NUMBER OF SEQ ID NOS: 934
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 535
/ LENGTH: 6082
/ TYPE: DNA
/ ORGANISM: Homo sapiens
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Pred. No.: 0
Score: 6760.00
Percent Similarity: 99.9%
Best Local Similarity: 99.9%
Query Match: 3
Matches: 6082
Conservative: 1324
Mismatches: 0
Indels: 1
Gaps: 0
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DB 246 CGCGTGTCTTCTGTGTGCTCATCTTGTTTAAATTTGGCATTAACGAGATTAGAG 305
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DB 306 GAAAGTGTATGTATTAATGATGCTGCAGAAAGCCCTCAGACGACCTTGAGAGAGATTG 365
QY 61 GlnGlyPheTrrPrrleuAsnLysGlnValleuArgAlaGluAsnAspAlaGlnLysProSerleu 80
DB 366 CAAAGGTTCTGGATTAAGAAAGCTTTTAAAGCTGGAATGACGACAGAGCTTCTTTA 425
QY 81 ThrArgAlallelleLysCysTyrTrrPrrleuValleuGlyllePheThrleu 100
DB 426 ACAAGAGCAATCATTAAGTGTACTGGAATCTTATTTAGTTTGGAAATTTTACGTTA 485
QY 101 lleGlnGluSerAlaleuValilleGlnProIlePheleuGlyLysIlelleAsnTyrPhe 120
DB 486 ATTTGAGAAAGTCCAAAGTATTCAGCCCAATTTTGGGAAAATTAATTAATTAATTTT 545
QY 121 GluAsnTyrAspProMetAspSerValAlaleuAsnThrAlaTyrAlaThrVal 140
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QY 181 leuSerAsnMetAlaMetGlyLysThrThrThrGlnIleValAsnleuSerAsn 200
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 US-09-651-236-535  
 / Sequence 535, Application US/09651236  
 / Patent No. 6818751  
 / GENERAL INFORMATION:  
 / APPLICANT: Xu, Jiangchun  
 / APPLICANT: Dillon, David C.  
 / APPLICANT: Mitchem, Jennifer L.  
 / APPLICANT: Harlocker, Susan L.  
 / APPLICANT: Jiang, Yuqi  
 / APPLICANT: Henderson, Robert A.  
 / APPLICANT: Kalos, Michael D.  
 / APPLICANT: Fanger, Gary R.  
 / APPLICANT: Retter, Marc W.  
 / APPLICANT: Stolk, John A.  
 / APPLICANT: Day, Craig H.  
 / APPLICANT: Vedic, Thomas S.  
 / APPLICANT: Carter, Darlick  
 / APPLICANT: Li, Samuel  
 / APPLICANT: Wang, Ajun  
 / APPLICANT: Skeiky, Yasir A.W.  
 / APPLICANT: Hepler, William  
 / TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 / FILE REFERENCE: 210121.42718C18  
 / CURRENT APPLICATION NUMBER: US/09/651,236  
 / NUMBER OF SEQ ID NOS: 865  
 / SOFTWARE: FastSeq for Windows Version 3.0  
 / SEQ ID NO 535  
 / LENGTH: 6082  
 / TYPE: DNA  
 / ORGANISM: Homo sapiens  
 / US-09-651-236-535  
 Alignment Scores:  
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 Percent Similarity: 99.98  
 Best Local Similarity: 99.98 Mismatches: 1  
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RESULT 9
US-10-012-896-535
; Sequence 535, Application US/10012896
; Patent No. 6943236
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Uiang, Yuguu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yaseir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.

```

APPLICANT: Houghton, Raymond L.  
 APPLICANT: Vinals de Bassols, Carlota  
 APPLICANT: Foy, Teresa  
 APPLICANT: Panger, Gary R.  
 APPLICANT: Mamanabe, Yoshinhiro  
 APPLICANT: Meagher, Madeleine Joy  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 FILE REFERENCE: 210121.427C27  
 CURRENT APPLICATION NUMBER: US/10/012,896  
 CURRENT FILING DATE: 2001-12-10  
 NUMBER OF SEQ ID NOS: 1011  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 535  
 LENGTH: 6082  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-10-012-896-535

## Alignment Scores:

Pred. No.: 0 Length: 6082  
 Score: 6760.00 Matches: 1324  
 Percent Similarity: 99.9% Conservative: 0  
 Best Local Similarity: 99.9% Mismatches: 1  
 Query Match: 99.6% Indels: 1  
 DB: 3 Gaps: 0

US-09-976-858-42 (1-1325) x US-10-012-896-535 (1-6082)

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Db 1986 AGTCAGATTCGTATATATGAAAGATGCTAAAGATGTCAGAGGGGCACTTACCTAGTTC 2045  
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Db 2046 CTAAATATCTGTATATATGATTTGGCTCCCTTTTAAAGAGATATAGAGAAAGTGAACA 2105  
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Qy 701 TyrLysAsnTyrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720  
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Qy 741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyLysAsnValThrGlnLysLeuAsp 760  
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Qy 761 LeuAsnTrpTyrLeuGlnGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780  
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Qy 801 MetPheGlnSerIleLeuLysAlaProValLeuPheAspArgAsnProIleGlyArg 820  
Db 2586 AGTTTGAATCAATTCGAAAGCTCCGGTATTAATCTTTGATAGAAATCCAAATAGGAAGA 2645  
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Db 3666 GATCTTCCCTGTAATATGATCTGAATTAAGCAGATCAGATTCCAATTTTGTGTGGA 3725  
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Qy 1261 LeuLeuGlnAsnLysGlnSerLeuPheTyrLysMetValGlnGlnLeuGlnLysValGln 1280  
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Qy 1301 GlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIle 1320  
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 DB 4145 TTCGAGACGACGACTG 4159  
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 US-09-439-313-536  
 ; Sequence 536, Application US/09439313  
 ; Patent No. 6329505  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Dillon, Davin C.  
 ; APPLICANT: Mitcham, Jennifer L.  
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 ; APPLICANT: Jiang Yugu  
 ; APPLICANT: Reed, Steven G.  
 ; APPLICANT: Kados, Michael  
 ; APPLICANT: Fanger, Gary  
 ; APPLICANT: Retter, Mark  
 ; APPLICANT: Solk, John  
 ; APPLICANT: Day, Craig  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
 ; FILE REFERENCE: 210121.427C9  
 ; CURRENT APPLICATION NUMBER: US/09/439,313  
 ; CURRENT FILING DATE: 1999-11-12  
 ; NUMBER OF SEQ ID NOS: 575  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 536  
 ; LENGTH: 6140  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: unsure  
 ; LOCATION: (4535)  
 ; OTHER INFORMATION: n=A,T,C or G  
 ; US-09-439-313-536  
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 Pred. No.: 0 Length: 6140  
 Score: 6600.50 Matches: 1300  
 Percent Similarity: 97.0% Conservative: 0  
 Best Local Similarity: 97.0% Mismatches: 0  
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 DB 775 GATCAGGAGACAGTTCCTTACCTTCCTGGGACAGACCACTGACGAGCGCATGCACTG 834  
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 QY 246 IleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSerLeuArgSerLysThr 265  
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QY 1290 ----- 1290  
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QY 1291 -----ValTyrPheLysArgAsnTyrProHisIleGlyHisThrAspHisMet 1306  
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RESULT 11  
US-09-636-215-536  
Sequence 536, Application US/09636215  
Parent No. 6620922  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, David C.  
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APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yuqi  
APPLICANT: Henderson, Robert A.  
APPLICANT: Kaloos, Michael D.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Retter, Marc W.  
APPLICANT: Stolk, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedyick, Thomas S.  
APPLICANT: Carter, Derrick  
APPLICANT: Li, Samuel  
APPLICANT: Mang, Aijun  
APPLICANT: Skeiky, Yaseir A.W.  
APPLICANT: Hepier, William  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.4271C17  
CURRENT APPLICATION NUMBER: US/09/636,215  
CURRENT FILING DATE: 2000-08-10  
NUMBER OF SEQ ID NOS: 852  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 536  
LENGTH: 6140  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(6140)  
OTHER INFORMATION: n=a,T,C or G  
US-09-636-215-536

Alignment Scores:  
Pred. No.: 0 Length: 6140  
Score: 6600.50 Matches: 1300  
Percent Similarity: 97.04 Conservative: 0  
Best Local Similarity: 97.04 Mismatches: 0  
Query Match: 97.34 Indels: 40  
DB: 3 Gaps: 1  
US-09-976-858-42 (1-1325) x US-09-636-215-536 (1-6140)

QY 26 TrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGlnIleAspMetTyr 45  
Db 225 TGGCTCAATCCCTTCTTTAAATTTGGCCATTAACCGAGATTTAGAGAGATATATGTAT 294  
QY 46 SerValIleuProGluAspArgSerGlnHisLeuGlyGluGlnLeuGlnGlyPheTyrAsp 65  
Db 225 TCAGTGTGCGCCAGAAAGACCGCTCACAGCACTTGGAGAGAGAGATTGCAAGGGCTTCGGAT 354  
QY 66 LysGluValIleuArgAlaGlnAsnAspAlaGlnLysProSerLeuThrArgAlaIle 85  
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QY 86 LysCysTyrTrpLysSerTyrLeuValIleuGlyIlePheThrLeuIleGluGlnSerAla 105  
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QY 106 LysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPheGluAsnTyrAspPro 125  
Db 475 AAAGTAAATCCAGCCCATTTTGGGAAAAATTAATTAATTTTGAATAATATGATCCC 534  
QY 126 MetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrValLeuThrPheCysThr 145  
Db 535 ATGATTTCTGTGGCTTTAAACACAGCGTACCGCTATGCGCAGGTCTGACTTTTGGCAG 594  
QY 146 LeuIleLeuAlaIleLeuHisIleLeuTyrPheTyrHisValGlnCysAlaGlyMetArg 165  
Db 595 CTGATTTTGGCTATCTGATCATCATTAATTTTATACGTTCACTGTGCTGGATGAG 654  
QY 166 LeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArgLeuSerAsnMetAla 185  
Db 655 TTACAGAGAGCCATGTGCAATATGATTTATCGAAGGACACTTGCTTAATAGTAACGTG 714  
QY 186 MetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsnAspValAsnLysPhe 205  
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QY 206 AspGlnValThrValPheLeuHisIlePheLeuThrAlaGlyProLeuGlnAlaIleAlaVal 225  
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QY 246 IleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSerLeuArgSerLysThr 265  
Db 895 ATTCCTCGCCCTTGCAAAAGCTGTTTGGGAAAGTTGCTCATCATCAAGAGGTAAACT 954  
QY 266 AlaThrPheThrAspAlaArgIleArgThrMetAsnGlnValIleThrGlyIleArgIle 285  
Db 955 GCACTTTCAAGATGACGAGATCAGACCATGAAATGAATTAATTAATCTGRTTAAGGATA 1014  
QY 286 IleLysMetTyrAlaTyrGluLysSerPheSerAsnLeuIleThrAsnLeuArgLysLys 305  
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 QY 566 ASPALAGLIVALSERARGHISLEUPHEGLULEUCYSILECYSGINILLEUHIISGLULYS 585  
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 QY 586 ILETHRILLEUVALTHRHSISGLINLEUGINTRYRLEULYSALASERGINILLEULEUI 605  
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Db 2395 AATGTCACTGTAAATGAGAGAGAAATGTAAACGAAAGCTAGATCTTAAGCTGTACTTA 2454  
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QY 1126 LeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlnHisThrAspGluGlu 1145  
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 QY 1146 LeuTPAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGluAspLeuProGlyLys 1165  
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 QY 1226 CysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAspSerAspLysIleMet 1245  
 DB 3835 TGCACCGTGTACCATTCGACACAGATTGAACACCATATTGACAGCGACAGATTAATG 3894  
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 QY 1291 -----ValTyrPheLysArgAsnTyrProHisIleGlyHisThrAspHisMet 1306  
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 US-09-685-166A-536  
 ; Sequence 536, Application US/09685166A  
 ; Patent No. 6630305  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Dillon, Devin C.  
 ; APPLICANT: Mitcham, Jennifer L.  
 ; APPLICANT: Harlocker, Susan L.  
 ; APPLICANT: Jiang, Yuqi  
 ; APPLICANT: Henderson, Robert A.  
 ; APPLICANT: Kalos, Michael D.  
 ; APPLICANT: Fanger, Gary R.  
 ; APPLICANT: Retter, Marc W.  
 ; APPLICANT: Stolk, John A.  
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 ; APPLICANT: Wang, Aijun  
 ; APPLICANT: Skeiky, Yabir A.W.  
 ; APPLICANT: Hepler, William  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.427C21  
 ; CURRENT APPLICATION NUMBER: US/09/685,166A  
 ; CURRENT FILING DATE: 2000-10-10  
 ; NUMBER OF SEQ ID NOS: 898  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 536  
 ; LENGTH: 6140  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1) ... (6140)  
 ; OTHER INFORMATION: n=A,T,C or G  
 US-09-685-166A-536  
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 US-09-976-858-42 (1-1325) x US-09-685-166A-536 (1-6140)  
 QY 26 TripleAsnProLeuPheLysIleGlyHisLysArgArgLeuGluLysAspMetTyr 45  
 DB 235 TGGCTCAATCCCTGTTTAAATTTGGCCATTAACGAGATTAAGAGAAATATATAT 294  
 QY 46 SerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeuGlnGlyPheThrAsp 65  
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 DB 355 AAAGAAATTTTAAAGCTGAGAAATGACGACAGAAAGCTTTTAAAGAAATTCATA 414  
 QY 86 LysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeuIleGluGlnSerAla 105  
 DB 415 AAGTTTACTGAAATCTTATTTAGTTTGGAAATTTTACGTTAATGAGAAAGTGCC 474  
 QY 106 LysValIleGlnProIlePheLeuGlyLysIleIleAsnTyrPheGluAsnTyrAspPro 125  
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 QY 146 LeuIleLeuAlaIleLeuHisIleLeuTyrPheTyrHisValGlnCysAlaGlyMetArg 165  
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 QY 246 IleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSerLeuArgSerLysThr 265  
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QY	266	AlaThrPheThrAspAlaArgIleArgThrMetLeuGluValIleThrGlyIleLeuArgIle	285
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QY	286	IleLeuMetIYrAlaTrpGluLeuSerPheSerAsnLeuIleThrAsnLeuArgIleLeu	305
Db	1015	ATAAAAATGTCACGCTGGGAAAAAGTCATTTTTCAAATCTTATTACCAATTTTGAAAGAAAG	1074
QY	306	GluIleSerIYleLeuArgSerSerCysIleuArgGlyMetAsnLeuAlaSerPhePhe	325
Db	1075	GAGATTTCCAGATTCGATCGAAGAGTTCTGTGCTCAGGGGAGATCAATTTGGCTCTTTTTC	1134
QY	326	SerAlaSerIYleIleValPheValThrPheThrTrpTrpValLeuLeuGlySerVal	345
Db	1135	AGTGCAACCAAAATCATCGTGTGTGTGACCTTCACACCTCAAGTACTCTCGGCAGTGTG	1194
QY	346	IleThrAlaSerArgValPheValAlaValThrLeuTrpGlyValAlaArgLeuThrVal	365
Db	1195	ATCACAGCACGCGGCTGTTCGTGGCAAGTACGCTGTATGGGGCTGTGCGGCTGACGGTT	1255
QY	366	ThrIleuPhePheProSerAlaIleGluArgValSerGluAlaIleValSerIleArgArg	385
Db	1255	AACCTCTTCTCCCTCAGCCATGAGAGGGGTGACAGGCGCATGTCAGATCCGAGAGA	1314
QY	386	IleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsnArgGlnLeuProSerAsp	405
Db	1315	ATCCAGACCTTTTCTCTCATGATGAGATATCACGCGCAACCGTCAGCTGCCGTCAGAT	1374
QY	406	GlyIYleuSerMetValHisValGlnAspPheThrAlaPheTrpAspIYleAlaSerGluThr	425
Db	1375	GGTAAAAAGATGTCATGTCAGAGATTTTACTGCTTTTGGGATTAAGCATCAAGACC	1434
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Db	1435	CCAATCTACAAAGGCTTTCCTTTACTGTCAACCTGGGGAATGTGTAGCTGTGATCGCG	1494
QY	446	ProValIleGlyAlaGlyIYleuSerSerLeuLeuSerAlaValLeuGlyGluLeuAlaProSer	465
Db	1495	CCCGTGGGAGCGAGGAAGTCATCAGCTGTTAAGTGTGCTCGGGGAATTTGGCCCCAAGT	1554
QY	466	HisGlyLeuValSerValHisGlyArgIleAlaTrpValSerGlnGluProThrValPhe	485
Db	1555	CACGGAGCTGTGACGGTCATGGAAGAAATGGCTATGATGTCACAGAGCCCTGGGATGTTT	1614
QY	486	SerGlyThrLeuArgSerAsnIleLeuPheGlyIYleuSerGlyIleuSerGluArgTrpGlu	505
Db	1615	TCCGGAACCTCGAGCAGTAAATTTTATTTTGGGAAGAAATACGAAGAAAGCAATATGAA	1674
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Db	1675	AAAGTCATTAAGGCTTTGTCTCTCGAAAAAGATTTTACAGCTGTGGAGGATGTTGATCTG	1734
QY	526	ThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnIYleuAlaArgValAsnLeu	545
Db	1735	ACTGTGATAGGAGATCGGGGAACACGCTGAGTGGAGGGGCAAGAAACACAGGGTAAACCTT	1794
QY	546	AlaArgAlaValTrpGlnAspAlaAspIleTrpLeuLeuAspAspProLeuSerAlaVal	565
Db	1795	GCAAGACGAGTATCAAGATCTCATCTTATCTCTGGAGATCTCTCATGTGCAGTA	1854
QY	566	AspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGlnIleLeuHisGluIYleu	585
Db	1855	GATGCGGAATTAGCAGACACTTGTTCGAACGTGTGATTTGTTCAAATTTTGCATGAGGAAG	1914
QY	586	IleThrIleLeuValThrHisGlnLeuGlnTrpLeuIYleuAlaAlaSerGlnIleLeuIle	605
Db	1915	ATCACAAATTTTATGTGCTCATCAGTTGCAGTACCTTCAAAAGCTGCAGATCAGATTTTGATA	1974
QY	606	LeuIYleuAspGlyIYleuMetValGlnIYleuGlyTrpTrpTrpGluPheLeuIYleuSerGlyIle	625
Db	1975	TTGAAAGATGTGTAATTTGGTGCAGAAAGGGGACCTTACACTGAAGTTCTTAAATCTGGTATA	2034
QY	626	AspPheGlySerLeuLeuIYleuIYleuAspAsnGluSerGluGlnProThrValProGly	645

Db	2035	GATTTTGGCTCCCTTTAAAGAAAGNAAAGAGAAAGTGAACAACCTCCAGTTCCAGCA	2094
OY	646	ThiProThrLeuArgAnaArgThrPheSerGluSerSerValTrpSerGlnGlnSerSer	665
Db	2095	ACTCCCAACACATAAGGAATCGTACCTTCTCAGAGCTTCGGTTGGTCTCAACAATCTTCT	2154
OY	666	ArgProSerLeuLeuAspGlyAlaLeuGluSerGlnAspThrGlnuAsnValProValThr	685
Db	2155	AGACCCCTCTTGAAAGATGGTGCTCTGGAAAGCCAAATACAGAAATGTCCACAGTTACA	2214
OY	686	LeuSerGlnGluuAsnArgSerGlnGlyLeuValGlyPheGlnAlaTrpLysAsnTrpPhe	705
Db	2215	CTATTCAGAGAGAACCTTCTCGAAGAAAGTTGGTTTCAAGCGCTATAAGAAATTACTTC	2274
OY	706	ArgAlaGlyAlaHisTrpLileValPheIlePheLeuIleLeuLeuAsnThrAlaGln	725
Db	2275	AGAGCTGTGTCTCACTGGAATGTCTTCAATTTCTTATTTCTCTTAACACATCGACGCTCAG	2334
OY	726	ValAlaTrpValLeuGlnAspTrpTrpLeuSerTrpTrpAlaAsnLysGlnSerMetLeu	745
Db	2335	GTTCGCCATATGCTTCAAGATGGTGCTTTCATACCTGGGCAACAAACAAAGATGTCTA	2394
OY	746	AsnValThrValaAsnGlyGlyLysAsnValThrGlnLysLeuAspLeuAsnTrpTrpLeu	765
Db	2395	AAATGTACTGTAAATGAGAGAGAAATGTAAACGAGAACCTAGATCTTAATCTGTACTTA	2454
OY	766	GlyIleTrpSerGlyLeuThrValAlaThrValLeuPheGlyIleAlaArgSerLeuLeu	785
Db	2455	GGAAATTAATTCAGGTTTAACGTAGTACCGTTCTTTTGGCATAGCAAAATCTCTATTTG	2514
OY	786	ValPheTrpValLeuValaAsnSerSerGlnThrLeuHisAsnLysMetPheGluSerIle	805
Db	2515	GTATTTCTTACGCTCTTGTAACCTCTTCCAAACTTGTGACAAACAAAGTTTGGATCAAT	2574
OY	806	LeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArgIleLeuAsnArgPhe	825
Db	2575	CTGAAAGCTCCGATTAATTTCTTTGATAGAAATCCATAGAGAAATTTTAATTCGTTTC	2634
OY	826	SerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPheLeuAspPheIleGln	845
Db	2635	TCCAAAGACATTTGACACTTGGATGATTTGGTCGCGCTGACGTTTAAAGATTTCATCAG	2694
OY	846	ThrLeuLeuGlnValValGlyValaLysValaValaValaValaIleProTrpIleAla	865
Db	2695	ACATTTGTCTACAGAGGTGGTGGTGTCTGTGTGCTGTGGCCGTGAATTCCTTGATGTCA	2754
OY	866	IleProLeuValProLeuGlyIleIlePheIlePheLeuArgArgTrpPheLeuGluThr	885
Db	2755	ATACCCTTGGTTCCTCGAATACATTTTCAATTTTCTTGCGCATAATTTTGGAAACG	2814
OY	886	SerArgAspValLysArgLeuGluSerThrThrArgSerProValPheSerHisLeuSer	905
Db	2815	TCAGAGAGTGGAAAGCGCGCTGGATCTACAACTGGAGTCCAGTGGTTTCCCACTTGCA	2874
OY	906	SerSerLeuGlnGlyLeuTrpThrIleArgAlaTrpLysAlaGlyGlnuArgGlyGlnGlu	925
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RESULT 13  
 US-09-679-426-536  
 / Sequence 536, Application US/09679426  
 / Patent No. 6759515  
 / GENERAL INFORMATION:  
 / APPLICANT: Xu, Jianshun  
 / APPLICANT: Dillon, Davin C.  
 / APPLICANT: Mitchem, Jennifer L.  
 / APPLICANT: Harlocker, Susan L.  
 / APPLICANT: Jiang, Yuqi  
 / APPLICANT: Henderson, Robert A.  
 / APPLICANT: Kalos, Michael D.  
 / APPLICANT: Renger, Gary R.  
 / APPLICANT: Retter, Marc W.  
 / APPLICANT: Stolk, John A.  
 / APPLICANT: Day, Craig H.  
 / APPLICANT: Vedrick, Thomas S.  
 / APPLICANT: Carter, Darlick  
 / APPLICANT: Li, Samuel  
 / APPLICANT: Wang, Aijun  
 / APPLICANT: Skeiky, Yasir A.W.  
 / APPLICANT: Hepler, William  
 / TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 / FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
 / FILE REFERENCE: 210121.427C20  
 / CURRENT APPLICATION NUMBER: US/09/679,426  
 / CURRENT FILING DATE: 2000-10-02  
 / NUMBER OF SEQ ID NOS: 895  
 / SOFTWARE: FastSeq for Windows Version 3.0  
 / SEQ ID NO 536  
 / LENGTH: 6140  
 / TYPE: DNA  
 / ORGANISM: Homo sapiens  
 / FEATURE:  
 / NAME/KEY: misc feature  
 / LOCATION: (1) ..(6140)  
 / OTHER INFORMATION: n-A,T,C or G  
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 Score: 6600.50 Matches: 1300  
 Percent Similarity: 97.0% Conservative: 0  
 Best Local Similarity: 97.0% Mismatches: 0  
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 Qy 66 LysGluValIleuArgAlaGluAsnAspAlaGluYrProSerLeuThrArgAlaIleIle 85  
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## RESULT 14

US-09-759-143-536  
Sequence 536, Application US/09759143  
Patent No. 6800746

## GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yugu  
APPLICANT: Henderson, Robert A.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Retter, Marc W.  
APPLICANT: Stolk, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedrick, Thomas S.  
APPLICANT: Carter, Derrick  
APPLICANT: Li, Samuel  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Hepler, William  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.427C23  
CURRENT FILING DATE: US/09/759,143  
CURRENT FILING DATE: 2001-01-12  
NUMBER OF SEQ ID NOS: 934  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO: 536  
LENGTH: 6140  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)\_(6140)  
OTHER INFORMATION: n=A,T,C or G  
US-09-759-143-536

## Alignment Scores:

Pred. No.:	0	Length:	6140
Score:	6600.50	Matches:	1300
Percent Similarity:	97.08	Conservative:	0
Best Local Similarity:	97.08	Mismatches:	0
Query Match:	97.38	Indels:	40
DB:	3	Gaps:	1

US-09-976-858-42 (1-1325) x US-09-759-143-536 (1-6140)

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 US-09-651-236-536  
 ; Sequence 536, Application US/09651236  
 ; Patent No. 6818751  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, Jianshun  
 ; APPLICANT: Dillon, Devin C.  
 ; APPLICANT: Mitcham, Jennifer L.  
 ; APPLICANT: Harlocker, Susan L.  
 ; APPLICANT: Jiang, Yugu  
 ; APPLICANT: Henderson, Robert A.  
 ; APPLICANT: Kalos, Michael D.  
 ; APPLICANT: Fanger, Gary R.  
 ; APPLICANT: Retter, Marc W.  
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 ; APPLICANT: Li, Samuel  
 ; APPLICANT: Wang, Aijun  
 ; APPLICANT: Skeiky, Yasir A.W.  
 ; APPLICANT: Hepler, William



1 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
2 FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
3 FILE REFERENCE: 210121.42718C18  
4 CURRENT APPLICATION NUMBER: US/09/651,236  
5 CURRENT FILING DATE: 2000-08-29  
6 NUMBER OF SEQ ID NOS: 865  
7 SOFTWARE: FastSeq for Windows Version 3.0  
8 SEQ ID NO 536  
9 LENGTH: 6140  
10 TYPE: DNA  
11 ORGANISM: Homo sapiens  
12 FEATURE:  
13 NAME/KEY: misc\_feature  
14 LOCATION: (1)...(6140)  
15 OTHER INFORMATION: n=A,T,C or G  
16 US-09-651-236-536  
  
17 Alignment Scores:  
18 Pred. No.: 0 Length: 6140  
19 Score: 6600.50 Matches: 1300  
20 Percent Similarity: 97.0% Conservative: 0  
21 Best Local Similarity: 97.0% Mismatches: 0  
22 Query Match: 97.3% Indels: 40  
23 Gaps: 1  
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25 US-09-976-858-42 (1-1325) x US-09-651-236-536 (1-6140)  
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 QY 646 ThrProThrLeuArgAsnArgThrPheSerGluSerSerValTrpSerGlnInserSer 665  
 DB 2095 ACTCCACACTAAGAAATGTAACCTTCTCAGAGTCTTCGGTTGGCTCAACAATCTTCT 2154  
 QY 666 ArgProSerLeuLysAspGlyValAlaGluSerGlnAspThrGluAsnValProValThr 685  
 DB 2155 AACACCTCTTAAAGATGTCCTCGAGAGCCCAAGATACAGAGATGTCACAGTTACA 2214  
 QY 686 LeuSerGluGluAsnArgSerGluGlyLysValGlyPheGlnAlaTrpLysAsnTrpPhe 705  
 DB 2215 CTAATCAGAGAGAAACCGTCTCAGAGAAAGTTGGTTTCAAGCCCTAATAGATTTACTTC 2274  
 QY 706 ArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeuAsnThrAlaAlaGln 725  
 DB 2275 AAGAGCTGGTCACTGATGTCCTTCAATTTCTTAACTCTTAAACACTGACAGCTCAG 2334  
 QY 726 ValAlaTrpValLeuGlnAspTrpTrpLeuSerTrpTrpAlaAsnLysGlnSerMetLeu 745  
 DB 2335 GTTGCCTATGTCCTTCAAGATTTGGCTTCACTGAGCAAAACAAGATATGCTA 2394  
 QY 746 AsnValThrValAsnGlyValLysAsnValThrGluLysLeuAspLeuAsnTrpTrpLeu 765  
 DB 2395 AATGCACTGTAAATGAGAGAGAAATGTAACCGAGAACTTGAATTTAACTGATCTTA 2454  
 QY 766 GlyIleTrpSerGlyLeuThrValAlaThrValLeuPheGlyIleAlaArgSerLeuLeu 785  
 DB 2455 GGAATTTATTCAGTTTAACTGATGTCCTTCTTTTGGCATGCAAGATCTGATATG 2514  
 QY 786 ValPheTrpValLeuValAsnSerSerGlnThrLeuHisAsnLysMetPheGluSerIle 805  
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 QY 806 LeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArgIleLeuAsnArgPhe 825  
 DB 2575 CTGAAGAGCTCCGGTATTATCTTGTATGAAATCCAAATGAGAAATTTTAAATCGTTTC 2634  
 QY 826 SerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPheLeuAspPheIleGln 845  
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 QY 886 SerArgAspValLysArgLeuGluSerThrThrArgSerProValPheSerHisLeuSer 905  
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 QY 906 SerSerLeuGlnGlyLeuTrpThrIleArgAlaTrpLysAlaGluGlnArgCysGlnGln 925  
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 QY 946 ArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheValIleIleValAlaPhe 965  
 DB 2995 CGCTGGTTCGCGCTCGCTGATGCAATCTGTGCATTTTGTATATATCGTTGCTTT 3054  
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QY 986 AlaLeuThrLeuMetGlyMetPheGlnTrpCysValArgInserAlaGluValGluAsn 1005  
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 QY 1106 ThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIleProGlnGluProVal 1125  
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 QY 1290 ----- 1290  
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 DB 4135 AGCCCAAGCTGAGATATCTTCAAAAGAAATTTATTCACATATTTGTGTCACTGACACAT 4194  
 QY 1306 ValThrAsnThrSerAsnGlyGlnProSerThrLeuThrIlePheGluThrAlaLeu 1325

Db 4195 GGTACAAACACTCTCCATGACAGCCCTCGACCTTACTATTTCGAGACAGCACTG 4252

Search completed: March 14, 2006, 13:53:46  
Job time : 763 secs

GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus.p2n model

Run on: March 14, 2006, 15:52:06 ; Search time 1653 Seconds  
(without alignments)  
1849.467 Million cell updates/sec

Title: US-09-976-858-42

Sequence: 1 MLPVQEVKRPMLDANIC.....MTNTNSQNPSTLITFETAL 1325

Scoring table:

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delpop 6.0 , Delpext 7.0	

Searched: 7673375 seqs, 1153648444 residues

Total number of hits satisfying chosen parameters: 15346750

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62  
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Database : Published Applications NA New:\*

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13:	/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Score	Query	Match	Length	ID	Description
No.						
1	6787	100.0	5716	12	US-11-124-367A-149	Sequence 149, App
2	6779	99.9	4231	7	US-10-329-258-9	Sequence 9, Appl
3	6760	99.6	6082	12	US-11-234-786-535	Sequence 535, App
4	6686	98.5	5875	12	US-11-091-883-414	Sequence 414, App

5	6600.5	97.3	6140	12	US-11-234-786-536	Sequence 536, App
6	3310.5	48.8	2143	12	US-11-124-367A-150	Sequence 150, App
7	3362	48.1	2256	12	US-11-124-367A-148	Sequence 148, App
8	2285.5	33.7	5011	7	US-10-826-585-35	Sequence 35, Appl
9	2285.5	33.7	5011	7	US-11-045-578-3	Sequence 3, Appl
10	2263	33.3	4587	12	US-11-045-578-2	Sequence 2, Appl
11	2235	32.9	4599	12	US-11-045-578-1	Sequence 1, Appl
12	2227	32.8	4551	7	US-10-933-182A-484	Sequence 484, App
13	2227	32.8	4551	7	US-10-933-182A-484	Sequence 484, App
14	2201	32.4	4954	12	US-11-136-527-2145	Sequence 2145, App
15	2174	32.0	5189	12	US-11-136-527-475	Sequence 475, App
16	2087	30.7	6129	7	US-10-501-035-124	Sequence 124, App
17	2087	30.7	6129	9	US-11-206-139-1	Sequence 1, Appl
18	2087	30.7	6129	9	US-11-127-832-24	Sequence 24, Appl
19	2052	30.2	5762	12	US-11-136-527-489	Sequence 489, App
20	2037.5	30.0	5139	12	US-11-132-864-47	Sequence 47, Appl
21	2037.5	30.0	5143	12	US-11-054-168B-20	Sequence 20, Appl
22	1988	29.3	3918	9	US-11-096-568A-29801	Sequence 29801, A
23	1887.5	27.8	4434	7	US-10-933-182A-76875	Sequence 76875, A
24	1887.5	27.8	4434	7	US-10-933-182A-76875	Sequence 76875, A
25	1867	27.5	4986	7	US-10-933-182A-1658	Sequence 1658, App
26	1867	27.5	4986	7	US-10-933-182A-1658	Sequence 1658, App
27	1843.5	27.2	4686	7	US-10-933-182A-3096	Sequence 3096, App
28	1843.5	27.2	4686	7	US-10-933-182A-3096	Sequence 3096, App
29	1825	26.9	4680	7	US-10-933-182A-191051	Sequence 191051, A
30	1825	26.9	4680	7	US-10-933-182A-191051	Sequence 191051, A
31	1802.5	26.6	5792	12	US-11-136-527-2846	Sequence 2846, App
32	1760	25.9	4826	12	US-11-030-439-23	Sequence 23, Appl
33	1748	25.8	4977	12	US-11-030-439-25	Sequence 25, Appl
34	1661	24.5	3357	7	US-10-933-182A-80104	Sequence 80104, A
35	1661	24.5	3357	7	US-10-933-182A-80104	Sequence 80104, A
36	1650.5	24.3	4999	8	US-10-995-561-10	Sequence 10, Appl
37	1649	24.3	5064	8	US-10-995-561-9	Sequence 9, Appl
38	1557.5	22.9	3910	8	US-10-995-561-451	Sequence 451, App
39	1543.5	22.7	2682	7	US-10-933-182A-5556	Sequence 5556, App
40	1543.5	22.7	2682	7	US-10-933-182A-5556	Sequence 5556, App
41	1537.5	22.7	3001	12	US-11-136-527-1015	Sequence 1015, App
42	1408	20.7	4863	12	US-11-128-049-958	Sequence 958, App
43	1408	20.7	4863	12	US-11-128-049-958	Sequence 958, App
44	1241.5	18.3	3243	7	US-10-933-182A-81883	Sequence 81883, A
45	1241.5	18.3	3243	7	US-10-933-182A-81883	Sequence 81883, A

#### ALIGNMENTS

RESULT 1  
US-11-124-367A-149  
; Sequence 149, Application US/11124367A  
; Publication No. US20060024700A1  
GENERAL INFORMATION:  
APPLICANT: Michele Cargill  
TITLE OF INVENTION: Genetic Polymorphisms Associated with  
FILE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof  
FILE REFERENCE: CL001519.ORD  
CURRENT APPLICATION NUMBER: US/11/124,367A  
CURRENT FILING DATE: 2005-05-09  
PRIOR APPLICATION NUMBER: US 60/568,846  
PRIOR FILING DATE: 2004-05-07  
PRIOR APPLICATION NUMBER: US 60/582,609  
PRIOR FILING DATE: 2004-06-25  
PRIOR APPLICATION NUMBER: US 60/599,554  
NUMBER OF SEQ ID NOS: 34460  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 149  
; TYPE: DNA  
; LENGTH: 5716  
; ORGANISM: Homo Sapiens  
US-11-124-367A-149  
Alignment Scores: 0 Length: 5716  
Pred. No.: 0

Score: 6787.00 Matches: 1325  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 12 Gaps: 0

US-09-976-858-42 (1-1325) x US-11-124-367A-149 (1-5716)

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 QY 21 ArgValPhePheTyrTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGln 40  
 DB 61 CGGCTGTTCTTCTGGTGGCTCAATCCCTGTTAAATTGGCCATTAACGAGATTAGAG 120  
 QY 41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60  
 DB 121 GAAGATGATATGATATTCAGTGTGCGAGAAACCGCTCAAGCACCTTGAGAGAGTTG 180  
 QY 61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80  
 DB 181 CAGGGTCTGGATTAAGAGAGTTTAAAGCTGAAGATGACGACAGAAAGCCTTCTTAA 240  
 QY 81 ThrArgAlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100  
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 DB 361 GAAATTAATGATCCAGATGATCTGTGCTTGAACAGCGACCGCATGCGACAGG 420  
 QY 141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisIleLeuTyrPheTyrHisValGln 160  
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 DB 481 TGTGCTGGGATGGGTTACGAGTAGCCATGTGCCAATGATTTATCGAAGGCACTTCGT 540  
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 DB 1321 TTAGCTGTGTGCGCCCGTGGAGACAGGAAATCATCATCTGTTAAGTCCGCTCGAG 1380  
 QY 461 GluLeuAlaProSerHisGlyLeuValSerValHisGlyAlaIleTyrValSerGln 480  
 DB 1381 GAATTGGCCCCAAGACAGGGGTGGTCAGCGTCAGTCGAGAAAGATTGCTATGTGCTCAG 1440  
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 DB 1441 CAGCCCTGGGTGTTCTCGGAACCTTGAGAGTAATATTTTATTTGGGAAAGAAATACAA 1500  
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 QY 641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGlnSerSerValTyr 660  
 DB 1921 CCTTCAGTTCCAGAACTCCCACTAAGAGATGTACTCTTCAGAGTCTTCGGTTGG 1980  
 QY 661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGlnSerGlnAspThrGlu 680  
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SOFTWARE: PatentIn version 3.1  
SEQ ID NO 9  
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TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (116)..(4093)  
OTHER INFORMATION:  
US-10-329-258-9

## Alignment Scores:

Pred. No.:	0	Length:	4231
Score:	6779.00	Matches:	1323
Percent Similarity:	99.9%	Conservative:	1
Best Local Similarity:	99.8%	Mismatches:	1
Query Match:	99.9%	Indels:	0
DB:	7	Gaps:	0

US-09-976-858-42 (1-1325) x US-10-329-258-9 (1-4231)

QY 1 MetLeuProValThrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20  
DB 116 ATGCTGCCGTGATCCAGAGGTTGAAGCCCAACCGCTGACAGACCGCAACATCTGCTCA 175  
QY 21 ArgValPhePheTrpTrpLeuAsnProLeuPheLysIleGlyHisLysArgArgLeuGln 40  
DB 176 CGCGGTTCTTCTGGTGGCTCAATCCCTTTAAATTTGGCATTAACGAGATTAAAG 235  
QY 41 GluAspAspMetLysSerValLeuProGluAspArgSerGlnHisLeuGlyGluGluLeu 60  
DB 236 GAAAGATGATATGATTCAGTGTCTGCAGAAAGCCGCTCACACACCTTGAGAGAGGTTG 295  
QY 61 GlnGlyPheTrpAspLysGluValLeuArgAlaGluAspAlaGlnLysProSerLeu 80  
DB 296 CAAAGGTTTGGATTAAGAAGTTTAAAGCTGAGAAATGACGACAGAAAGCTTTCTTTA 355  
QY 81 ThrArgAlaIleIleLysCysTrpTrpLysSerTrpLeuValLeuGlyIlePheThrLeu 100  
DB 356 ACAAGAGCAATCATTAAGTGTAACTGGAATCTTATTGTTTGGGAATTTTACGTTA 415  
QY 101 IleGluGlnSerAlaLysValIleGlnProIlePheLeuGlyLysIleIleAsnTrpPhe 120  
DB 416 ATTGAGAAAGTGCCCAAGTAATCCAGCCCATATTTTGGGAAAATTTATTAATTAATTT 475  
QY 121 GluAsnTrpAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaThrVal 140  
DB 476 GAAATATATGATCCCATGGAATCTGTGCTTGAACACAGCGTACCGCTATGACAGGTTG 535  
QY 141 LeuThrPheCysThrLeuIleLeuAlaIleLeuHisIleLeuTrpPheTrpHisValGln 160  
DB 536 CTGACCTTTTGCACGCTCATTTTGGCTATACAGCACTTATATTTTATCACGTTGAG 595  
QY 161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTrpArgLysAlaLeuArg 180  
DB 596 TGTGTGGGATAGAGTTACAGATGACCATGTGCATATGATTATTCGAAAGCACTTCGT 655  
QY 181 LeuSerAsnMetAlaMetGlyLysThrTrpThrGlnIleValAsnLeuSerAsn 200  
DB 656 CTTAGTAACATGCGCAGTGGAGAAAGACACACAGGCGAATGTCATCTGCTGCATCAT 715  
QY 201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220  
DB 716 GATGTGAACAAGTTTGTATCAGGTGACAGTGTCTTTCACCTTCGTGGGACAGGACCACTG 775  
QY 221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGly 240  
DB 776 CAGGCGATCGCAGTGACTGCCCTACTCTGATGAGATAGAAATATCGTCTGTGGG 835  
QY 241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260  
DB 836 ATGGAGGTTCTATATCTCTCCGCTTGCAAAAGCTGTTTGGGAAAGTTGTTCTCATCA 895

QY 261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgThrMetAsnGluValIle 280  
DB 896 CTGAGAGATTAAGCACTTTCACGATGCCAGATCAGACCATGAAATGAAGTTTATA 955  
QY 281 ThrGlyIleArgIleIleLysMetTrpAlaTrpGluLysSerPheSerAsnLeuIleThr 300  
DB 956 ACTGATTAAGGATATATTAATATGACCTCGGAAAAGTCAATTTTCAAACTTTATAC 1015  
QY 301 AsnLeuArgLysGluIleSerLysIleLeuArgSerSerCysLeuArgLysMetAsn 320  
DB 1016 AATTGGAAGAAAGAGGATTTCCAAAGATTCGAGAAATCTCTGCTCAGGGGGATGAT 1075  
QY 321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrTrpVal 340  
DB 1076 TTGGCTTGTGTTTTCAGTGCAAGCAAAATCATCGTGTGTCACCTTCAACCACTTACG 1135  
QY 341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTrpGlyAla 360  
DB 1136 CTCTCGGACAGTGATCACAGCCAGCCGCTGTTCTGAGCAGTACCTGTATGGGCT 1195  
QY 361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380  
DB 1196 GTGCGGCTGACGGTTACCTCTTCTCCCTCAGCATTTGAGAGGGTGTCAAGAGCAATC 1255  
QY 381 ValSerIleArgArgIleGlnThrPheLeuLeuAspGluIleSerGlnArgAsnArg 400  
DB 1256 GTCAAGATCCGAAGATCAGACCTTTTGGTACTGTATGATATCAAGGCAACCGT 1315  
QY 401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420  
DB 1316 CAGCTGCGTCAGATGATTAAGATGATGATGATGATGATTTTACGCTTTTGGGAT 1375  
QY 421 LysAlaSerGluThrProThrLeuGlnLysLeuSerPheThrValArgProGlyGluLeu 440  
DB 1376 AAGCATCAGAGACCCCAACTCTACAGGCTTTCTTACGTGACAGCTGGCAATTG 1435  
QY 441 LeuAlaValAlaGlyProValGlyValAlaGlyLysSerSerLeuLeuSerAlaValLeuGly 460  
DB 1436 TTAGCTGTGTGCGGCCCGTGGAGACAGGAAATCATCATCATGTTAAGCCGTCTCGG 1495  
QY 461 GluLeuAlaProSerHisGlyLeuValSerValHisValArgIleAlaTyrValSerGln 480  
DB 1496 GAATGGCCCCAAGTACAGGGGTGTGACGCTGATGAGAAATGCTTATGTGTCTGAG 1555  
QY 481 GlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTrpGlu 500  
DB 1556 CAGCCCTGGGTCTTCTCGGAACTCTGAGAGTATATTTATTTGGGAAAGAAATATGA 1615  
QY 501 LysGluArgTrpGluLysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeu 520  
DB 1616 AAGGAACGATATGAAGAAAGTCAATAAGGCTTGCTCGAAGAAAGATTTACAGCTGTG 1675  
QY 521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540  
DB 1676 GAGGATGTGATCTACTGTGTAGAGATCGGGGAAACCAAGCTGATGAGAGGAGGAGAA 1735  
QY 541 AlaArgValAsnLeuAlaArgAlaValTyrGlnAspAlaAspIleTyrLeuLeuAspAsp 560  
DB 1736 GCGCGGTTAACTTTCGAAGAGCACTGTATCAAGATGCTGACATCTACTCTGACCAT 1795  
QY 561 ProLeuSerAlaValAspAlaGluValSerArgHisLeuPheGlnLeuCysIleCysGln 580  
DB 1796 CCTCTCAGTGCAGTGATGCGGGAATGTAGACAGACCTTGTTGGAACGTGTGTTGTGCA 1855  
QY 581 IleLeuHisGlyLysIleThrIleLeuValThrHisGlnLeuGlnTrpLeuLysAlaIle 600  
DB 1856 AATTTCAGATGAGAAATACAAATTTTATGATCTATCAGTTGCACTTAACTGCA 1915  
QY 601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTrpThrGluPhe 620  
DB 1916 ACTCAGATTTCTATATTTGAAGATGTTAAATGTGTGACAGAGGAGCACTTACAGTTG 1975  
QY 621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGluGlnSerGluGln 640



Db 1976 CTAATATCGTATGATTTGGCTCCCTTTAAAGAGATTAAGAGAAAGTGAACA 2035  
 Qy 641 ProProValProGlyThrProThrLeuArgAsnGlyThrPheSerGluSerSerValTrp 660  
 Db 2036 CCTCAGATTCAGAGAACTCCCACTAAGAAATCGATCTTCAGAGCTTCGCGTTGG 2095  
 Qy 661 SerGlnGlnSerSerArgProSerLeuArgAspGlyAlaLeuGluSerGlnAspThrGlu 680  
 Db 2096 TCTCAACAAATCTTCAAGACCTTCCTGAAAGATGGCTCTGAGAGCCAAATACAGAG 2155  
 Qy 681 AsnValProValThrLeuSerGluGluAsnArgSerGluGlyValValGlyPheGlnAla 700  
 Db 2156 AATGCCCAAGTACACTATACAGAGAGAACCTTCGAAAGAAAGTTGTTTCAGGCG 2215  
 Qy 701 TyrLeuAsnThrPheArgAlaGlyAlaHisTrpIleValPheIlePheLeuIleLeuLeu 720  
 Db 2216 TATAAGAAATTAATCTCAGAGCTGCTGCTCAGATTTGCTTCATTTTCTTATTCCTCA 2275  
 Qy 721 AsnThrAlaAlaGlnValAlaTyrValLeuGlnAspTrpTrpLeuSerTyrTrpAlaAsn 740  
 Db 2276 AACACTGACGCTCAGAGTGGCTTAATGCTTCAAGATGGTGGCTTTCATACCTGGCAAC 2335  
 Qy 741 LysGlnSerMetLeuAsnValThrValAsnGlyGlyValAsnValThrGluLysLeuAsp 760  
 Db 2336 AACAAAGATATCTAAATGCTCACTGTAATGAGAGAGAAATGTAAACGAGAACTAGAT 2395  
 Qy 761 LeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780  
 Db 2396 CTTAATCGGTAATTAAGAAATTAATTAATCAGGTTTAATGTAAGTACGCTTCTTTTGGCAAT 2455  
 Qy 781 AlaArgSerLeuLeuValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLys 800  
 Db 2456 GCAAAATCTTAATGTATTTTACGCTCTGTAACTCTTCAAACTTGTGACAAACAA 2515  
 Qy 801 MetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAsnProIleGlyArg 820  
 Db 2516 ATGTTTGAATCTAATCTGAAGCTCCGGATTAATTTCTTTGATAGAAATCAATAGAGAA 2575  
 Qy 821 IleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeuLeuProLeuThrPhe 840  
 Db 2576 ATTTTAAATCGTTTCTCCAAAGACATTTGACACTTGGATGATTTGGTCCGCTGACGTTT 2635  
 Qy 841 LeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerValAlaValAlaVal 860  
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 Db 2876 GAGAGGTGTCAGAACTGTTTATATGACACAGAGATTTACATTCAGAGGCTTGGTCTTG 2935  
 Qy 941 PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal 960  
 Db 2936 TTTTGGACAAAGCTCCGCTGGTTCGCGCTCGCTCGATGCAATCTGTGCCAATGTTTGGC 2995  
 Qy 961 IleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAlaGlyGlnValGly 980  
 Db 2996 ATCATCGTTGCTTGGGATCCCTGATTCGGCAAAACCTGATGCCGGGACAGGTTGAT 3055  
 Qy 981 LeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGluTrpCysValArgGlnSer 1000

Db 3056 TTGGCACTGCTCATAGCCCTCAGCTCAGGAGATGTTTCAAGTGGTGTTCAGCAAAAGT 3115  
 Qy 1001 AlaGlyValGluAsnMetMetIleSerValGluArgValIleGluTyrThrAspLeuGlu 1020  
 Db 3116 GCTGAAGTGAAGATATATATATATCTCAGTAAGAAAGGATCATTTGATACAGACTTGAA 3175  
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 Db 3176 AAAGAGACCTTGGGAATATCAAGAAAGCCCAACAGCTGGCCCAATGAAGAGAGG 3235  
 Qy 1041 IleIlePheAspAsnValAsnPheMetTyrSerProGlyGlyProLeuValLeuLysHis 1060  
 Db 3236 ATTAATCTTGAACAATGTGAATCTTCATGACAGTCCAGCTGGGCTCTCTGTACTGAAGCAT 3295  
 Qy 1061 LeuThrAlaLeuIleLysSerGlnGluLysValGlyIleValGlyArgThrGlyValGly 1080  
 Db 3296 CTGACAGACCTCATTAATTAATCAAGAAAGGTTGGCATTTGGAGAAACCGAGACTGGA 3355  
 Qy 1081 LysSerSerLeuIleSerAlaLeuPheArgLeuSerGluProGluGlyLysIleTrpIle 1100  
 Db 3356 AAAAGTCCCTCATCTCAGCCCTTTTATGATTTGTCAGAACCCGAAGTAAATTTGGATT 3415  
 Qy 1101 AspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArgLysLysMetSerIleIle 1120  
 Db 3416 GATAAGATCTTGACAACTGAATTTGACCTTCACGATTTAAGAGAAATGTCATCATATA 3475  
 Qy 1121 ProGlnGluProValLeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlu 1140  
 Db 3476 CCTCAGAACTGTTTGTTCATCTGGAACAATGAGAAACCTGGAATCCCTTTAAGAGG 3535  
 Qy 1141 HisThrAspGluGluLeuTrpAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGlu 1160  
 Db 3536 CACACGATGAGAACTGTGAATGCTTCAAGAGGTACAACTTAAAGAAACCTTGA 3595  
 Qy 3596 GATCTTCTGGTAAATGATGATTCGAATTAAGAGATTCAGATTCATTTTATGTTTGA 3655  
 Db 1161 AspLeuProGlyLysMetAspThrGluLeuAlaGlnSerGlySerAsnPheSerValGly 1180  
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 Qy 1201 AspGluAlaThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArg 1220  
 Db 3716 GATGAAGAGAGGCAATGTGATTCAGAACTGATGCTTAATACAAAATAATCCGG 3775  
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 Db 3836 AGCGACAGATGATGTTTATGATTCAGAAAGACTGAAGAAATGATGACAGCCGTATGTT 3895  
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 Db 3896 TTGCTGCAAAATTAAGAGACCTATTTTACAGATGGTGCAACCACTGGGCAAGGACAGA 3955  
 Qy 1281 AlaAlaAlaLeuThrGluThrAlaLysGlnValTyrPheLysArgAsnTyrProHisIle 1300  
 Db 3956 GCCGCTGCCCTCAGCAAGCAACCAAAACAGATATCTTCAAAAGAAATTTATCCACATTT 4015  
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 Qy 1321 PheGluThrAlaLeu 1325  
 Db 4076 TTCGAGACGACCTG 4090

RESULT 3  
 US-11-234-786-535  
 ; Sequence 535, Application US/11234786

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Publication No. US20060024301A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuguu
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yaser A.
TITLE OF INVENTION: PROSTATE-SPECIFIC POLYPEPTIDES AND FUSION
FILE REFERENCE: 210121.427C31
CURRENT APPLICATION NUMBER: US/11/234,786
PRIOR APPLICATION NUMBER: US 09/568,857
PRIOR FILING DATE: 2000-05-09
PRIOR APPLICATION NUMBER: US 09/536,857
PRIOR FILING DATE: 2000-05-27
PRIOR APPLICATION NUMBER: US 09/483,672
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US 09/439,313
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: US 09/352,616
PRIOR FILING DATE: 1999-07-13
PRIOR APPLICATION NUMBER: US 09/288,946
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: US 09/232,149
PRIOR FILING DATE: 1999-01-15
PRIOR APPLICATION NUMBER: US 09/159,812
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: US 09/115,453
PRIOR FILING DATE: 1998-07-14
PRIOR APPLICATION NUMBER: US 09/030,607
PRIOR FILING DATE: 1998-02-25
Remaining Prior Application data removed - See File Wrapper or PALM.
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 535
LENGTH: 6082
TYPE: DNA
ORGANISM: Homo sapiens
US-11-234-786-535

Alignment Scores:
Pred. No.: 0 Length: 6082
Score: 6760.00 Matches: 1324
Percent Similarity: 99.9% Conservative: 0
Best Local Similarity: 99.9% Mismatches: 1
Query Match: 99.6% Indels: 1
DB: 12 Gaps: 0

US-09-976-858-42 (1-1325) x US-11-234-786-535 (1-6082)
QY 1 MetLeuProValTyrGlnGluValLysProAsnProLeuGlnAspAlaAsnLeuCysSer 20
DB 186 ATGCTGCCCGTGTATCCAGAGAGTGAAGCCCAACCGCTGACAGACGCAACTTCTGCTCA 245
QY 21 ArgValPhePheTrpTrpLeuAsnProLeuAsnPhelYsIleGlyHisLysArgArgLeuGln 40
DB 246 CCGGTGTCTTCTGCGGTGCTCAATCCCTGTTTAAATTGGCCATTAACGAGATTAGAG 305
QY 41 GluAspAsnMetLysSerValLeuProGluAspArgSerGlnHisLeuGlnYgluGluLeu 60
DB 306 GAAGATGATATGATTCAGTGTGCTGCCAAGACCGCTCAAGACCTTGGAAGAGATTGG 365
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QY 61 GlnGlyPheTrpAspArgLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80
DB 366 CAAAGGTTCTGGAGTAAAGAAAGTTTAAAGACTGAGTAGCGCACAGAACCTTCTTTA 425
QY 81 ThrArgAlaIleIleLysCysEtyrTrpLysSerTyrLeuValLeuGlyIlePheThrLeu 100
DB 426 ACAAGAGATCATTAAGTGTATCTGAGAACTTATTTAGTTTGGAAATTTTACGTTA 485
QY 101 IleGluGlnSerAlaLysValIleGlnProIlePheLeuGlyLysIleAsnTyrPhe 120
DB 486 ATTAGGAAGATGCCAAAGTATCATCGCCATATTTTGGGAAAAATTAATTAATTTT 545
QY 121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaThrVal 140
DB 546 GAAATATGATCCCATGATTCGTGCTTGAACACAGCGTACGCTATGCCACGGTGG 605
QY 141 LeuThrPheCysTrpTrpLeuIleLeuAlaIleLeuHisIleLeuTyrPheTyrHisValGln 160
DB 606 CTGACTTTTTCAGCTCATTTTGGCTATCTGATCATCATTAATTTTATCATCGTTGAG 665
QY 161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180
DB 666 TGTGCTGGAGTAGAGTTTACAGTAGTACCATGTCATATGATTTATCGAAGGCACTTGT 725
QY 181 LeuSerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuSerAsn 200
DB 726 CTTAGTAAATCATGGCCATGGGAGAGACACACAGGCCGAGATGCAATCTGCTGCCAT 785
QY 201 AspValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeu 220
DB 786 GATGTGAACAGATTGATCAGGTGACAGTGTCTTACCTTCTGTTGGGACGAGACCATG 845
QY 221 GlnAlaIleAlaValThrAlaLeuLeuTrpMetGlnIleGlyIleSerCysLeuAlaGly 240
DB 846 CAGGAGATCGCAGTACCTGCCCTACTCGATGAGATAGAAATATGCTGCTGCTGG 905
QY 241 MetAlaValIleLeuIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260
DB 906 ATGGCAGTTCTAATCATCTCTCGCCCTTGGAAGCTGTTTGGGAATGTTTCTTCATCA 965
QY 261 LeuArgSerLysThrAlaThrPheThrAspAlaArgIleArgTrpMetAsnGlnValIle 280
DB 966 CTGAGAGATTAAGATTAATAAATGTACCGCTGCGAGATCAGATCAGATCAATGATTA 1025
QY 281 ThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSerPheSerAsnLeuIleThr 300
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DB 1086 AATTGAGAAAGAAAGAGATTTCCAAGATTCGAGAAATTCCTGCTCAGCGGAGTAGAT 1145
QY 321 LeuAlaSerPhePheSerAlaSerLysIleIleValPheValThrPheThrThrTyrVal 340
DB 1146 TTGGCTGTGTTTTCAGTGCAAGCAAAATCATCGTTTGGACCTTCAACCACTTACGTG 1205
QY 341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360
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QY 361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGlnAlaIle 380
DB 1266 GTGGCGGTGACGGTTACCTCTTCTTCCCTCAGCAATGAGAGGCTGACAGAGCAATC 1325
QY 381 ValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGlnIleSerGlnArgAsnArg 400
DB 1326 GTCAACATCCGAAAGATCAGACCTTTTGTCTACTGTATGATATCAACAGGCAACCGT 1385
QY 401 GlnLeuProSerAspGlyLysLysMetValHisValGlnAspPheThrAlaPheTrpAsp 420
DB 1386 CAGTCCCGTCAAGATGTAAAGATGTGATGTGACAGATTTTACTGCTTTTGGGAT 1445
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QY 421 LysAlaSerGluThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyGluLeu 440  
DB 1446 AAGGATCAGAGACCCCAACTCTACAGGCCCTTCTTACTGTGAGACCTGGGAAATTG 1505  
QY 441 LeuAlaValGlyProValGlyAlaGlyLeuSerSerLeuLeuSerAlaValLeuGly 460  
DB 1506 TTAGCTGTGCTGGCCCGCTGGAGACAGAGAGTCACTGTTAAAGTCCGTGCTGGG 1565  
QY 461 GlnLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaThrValSerGln 480  
DB 1566 GAATGGGCCCCCAAGTCACGGCGCTGGTCAGCGTCAGAGAAATTGCCATGTGCTCG 1625  
QY 481 GlnProThrValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLeuSerTyrglu 500  
DB 1626 CAGCCCTGGGTCTTCTCGGAACTGTAGGACTAATTTTATTGGGAGAAATACGA 1685  
QY 501 LysGluArgTyrgluLeuValIleValAlaCysAlaLeuValLeuAspLeuGlnLeuLeu 520  
DB 1686 AAGGAACGATGTGAAAAAGTCATAAAGGCTGTGCTGAAAAAGATTACAGCTGTTG 1745  
QY 521 GluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLys 540  
DB 1746 GAGGATGGATCTACTGTGTAGAGAGATCGGGAAACCGCTGAGTGAAGGACAGAA 1805  
QY 541 AlaArgValAsnLeuAlaArgAlaValTyrglnAspAlaAspIleTyrLeuLeuAspAsp 560  
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QY 561 ProLeuSerAlaValAspAlaGlyValSerArgHisLeuPheGlyLeuCysIleCysGln 580  
DB 1866 CCTCAGTGCAGTAGATGCGGAGTTAGCAGACACTGTGTAACCTGTGTAATTTGTGCA 1925  
QY 581 IleLeuHisGlyLysIleThrIleLeuValThrHisGlnLeuGlnTyrLeuValAla 600  
DB 1926 ATTTTGCAATGAGAAATCACAATTTTAGTCACTCACTGCTCACTCACTCACTCACTGCA 1985  
QY 601 SerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGlnPhe 620  
DB 1986 AGTCGATTTCTGATTTGAAAGATGCTAAATGCTGACAGAGGGAACCTTACCTGAGTTC 2045  
QY 621 LeuLysSerGlyIleAspPheGlySerLeuLeuLysLysAspAsnGlyLysSerGln 640  
DB 2046 CTAATAATCTGGTATGATTTTGGCTCCCTTTAAAGAGATATGAGAAAGTGAACA 2105  
QY 641 ProProValProGlyThrProThrLeuArgAsnArgThrPheSerGlyLysSerValTyr 660  
DB 2106 CCTCAGTTCAGGAACTCCCACTCAAGAAATCGTACCTTCTCAGAGCTTCGGTTCG 2165  
QY 661 SerGlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGlnSerGlnAspThrGln 680  
DB 2166 TCTCAAAATCTTCTAGACCTCTCTTGAAGATGCTGCTGAGAGCCCAAGATACAGAG 2225  
QY 681 AsnValProValThrLeuSerGlyLysAsnArgSerGlyLysValGlyPheGlnAla 700  
DB 2226 AATGCCCAAGTATCACTATCAGAGGAAACGTTCTGAAGGAAAGTTGTTTCAGGCC 2285  
QY 701 TyrTyrAsnTyrPheArgAlaGlyAlaHisTyrPileValPheIlePheLeuIleLeuLeu 720  
DB 2286 TATAAAGATTAATCTCAGAGCTGGTCTCACTGATGTCTTCATTTTCTTATTTCTCTCA 2345  
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DB 2406 AAACAAAGATGCTAAATGCTCACTGTAATGAGAGGAAATGTAAACGAGAAAGCTAAGT 2465  
QY 761 LeuAsnTyrTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrValLeuPheGlyIle 780  
DB 2466 CTTAACGTGATCTTGAATTTATTCAGGTTTAACTGATCACTGACGTTCTTTTGGCATTA 2525  
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DB 2526 GCAAGATCTATTGATGATTTCTACGCTCTTAACTTCAACAACTTGACAAACAA 2585  
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DB 3366 CTGACAGCACTATTAAATCAAGAAAAAGTTGCAATTTGGAGAAACCGAGACTGGA 3425  
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DB 3486 GATAAGATCTTGACAACTGAAATTTGACCTTCACTGATTTAAAGAAATATGATCATATTA 3545  
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RESULT 4
US-11-091-883-414
; Sequence 414, Application US/11091883
; Publication No. US20060024693A1
; GENERAL INFORMATION:
; APPLICANT: CIBELLI, JOSE
; APPLICANT: FERNANDEZ, EMILIO O.
; APPLICANT: JORDAO DE MEGALHAES, GUILHERME
; APPLICANT: KOCABAS, ARIF
; APPLICANT: CROSBY, JAVIER A.
; TITLE OF INVENTION: IDENTIFICATION OF GENES OR POLYPEPTIDES THE EXPRESSION OF WHICH
; TITLE OF INVENTION: CORRELATES TO FERTILITY, OVARIAN FUNCTION AND/OR FETAL/NEBORN
; FILE REFERENCE: 53942US
; CURRENT APPLICATION NUMBER: US/11/091,883
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: 60/556,875
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 513
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 414
; LENGTH: 5875
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; ORGANISM: Homo sapiens
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; LOCATION: (5689)..(5689)
; OTHER INFORMATION: a, c, g, or t
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US-11-091-883-414

## Alignment Scores:

Pred. No.: 0 Length: 5875  
 Score: 6686.00 Matches: 1315  
 Percent Similarity: 99.14 Conservative: 1  
 Best Local Similarity: 99.04 Mismatches: 9  
 Query Match: 98.54 Indels: 3  
 DB: 12 Gaps: 0

US-09-976-858-42 (1-1325) x US-11-091-883-414 (1-5875)

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 QY 21 ArgValIlePhePheTrpLeuAsnProLeuPheIysIleGlyHisIleYsArgTrpLeuGlu 40  
 Db 176 CCGGTGTTCTTGAGGCTCAATCCCTGTTAAATGGCCATMAACGGAGATTAGAG 235  
 QY 41 GluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisIleuGlyGluLeu 60  
 Db 226 GAAAGATGATATATATTACGTGCTGCCAGAGACCGCTCACAGACCTTGAGAGAGATTG 295  
 QY 61 GInGlyPheTrpAspLysGluValLeuArgAlaGluAsnAspAlaGlnLysProSerLeu 80  
 Db 226 CAAGGTTCTGGATTAAGAAAGTTTAAAGAGCTGAGAAATGACGACAGAGAGCTTCTTTA 355  
 QY 81 ThrArgAlaIleIleIleYsCysPheTyrTrpLysSerTyrLeuValLeuGlyYIlePheTrpLeu 100  
 Db 356 ACAGAGCAATCATMAAGTTACTGGAATCTTATTAAATTGGAAATTTTATACGTTA 415  
 QY 101 IlegInuSerAlaIleValIleGlnProIlePheLeuGlyYsIleIleAsnTyrPhe 120  
 Db 416 ATTGAGAAAGGCCAAAGTATCCAGCCCATATTTTGGAAAAATTTATTAATTAATTTT 475  
 QY 121 GluAsnTyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaThrVal 140  
 Db 476 GAAATTTATGATCCCATGATTCTGTGGCTTTGAAACAGCGGTACGCCATGCCAGCGGTG 535  
 QY 141 LeuTrpPheCysThrLeuIleLeuAlaIleLeuHisIleIleuTyrPheTyrHisValGln 160  
 Db 536 CTGACTTTTGGACCGCTCATTTTGGCTATACGCACTCATTAATTTTATCACCGTCTAG 595  
 QY 161 CysAlaGlyMetArgLeuArgValAlaMetCysHisMetIleTyrArgLysAlaLeuArg 180  
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 QY 241 MetAlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSer 260  
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 QY 301 AsnLeuArgLysLysGluIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsn 320

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 Db 1076 TTGGCTGTGTTTTCAGTGCAAGCAAAATCATGTTGTGACCTTCAACCACTTACGTTG 1135  
 QY 341 LeuLeuGlySerValIleThrAlaSerArgValPheValAlaValThrLeuTyrGlyAla 360  
 Db 1136 CTCCCTGGCAGTGTATCAGACGCGCGGTGTTGTTGGCAGTACGCTGTATGGGGCT 1195  
 QY 361 ValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIle 380  
 Db 1196 GTGCGCTGACGCGTTACCTCTTCTTCCCTCAGCCATTTGAGAGGGGTGACAGAGCAATC 1255  
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 QY 480 InGlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTyrG 500  
 Db 1556 AGCAGCCTGTGTGTCTGGGAACCTGAGAGATTAATTTATTTGGAAAGAAATATG 1615  
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 Db 3896 TTTTGCTGAAATTAAGAGACCTATTTTACAAAGTGTGCAACAACCTGGCAAGCGCAG 3955  
 Qy 1280 LuAlaAlaLeuThrGluThrAlaLysGlnVal-TyrPheLysArgAsnTyrProHis 1299  
 Db 3956 AAGCGCTCCCTCACTGAAACAGCAAAACAGTAAATCTTCAAAAGAAATTAATCCACT 4015  
 Qy 1300 LLeGlyHisThrAspHisMetValThrAsnThrSerAsnGlyGlnProSerThrLeuThr 1319  
 Db 4016 ATTTGTCACATGCAACCAATGTTTACAAACACTTCCAAATGACAGCCCTGACCTTAAC 4075  
 Qy 1320 LLePheGluThrAlaLeu 1325  
 Db 4076 ATTTTGAAGACGACTG 4093

## RESULT 5

US-11-234-786-536

; Sequence 536, Application US/11234786

; Publication No. US20060024301A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuguu

; APPLICANT: Reed, Steven G.

; APPLICANT: Kalo, Michael D.

```

APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darriek
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yael A.
TITLE OF INVENTION: PROSTATE-SPECIFIC POLYPEPTIDES AND FUSION
FILE OF INVENTION: POLYPEPTIDES THEREOF
FILE REFERENCE: 210121.427C31
CURRENT APPLICATION NUMBER: US/11/234,786
CURRENT FILING DATE: 2005-09-23
PRIOR APPLICATION NUMBER: US 09/568,857
PRIOR FILING DATE: 2000-05-09
PRIOR APPLICATION NUMBER: US 09/536,857
PRIOR FILING DATE: 2000-05-27
PRIOR APPLICATION NUMBER: US 09/483,672
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US 09/439,313
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: US 09/352,616
PRIOR FILING DATE: 1999-07-13
PRIOR APPLICATION NUMBER: US 09/288,946
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: US 09/232,149
PRIOR FILING DATE: 1999-01-15
PRIOR APPLICATION NUMBER: US 09/159,812
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: US 09/115,453
PRIOR FILING DATE: 1998-07-14
PRIOR APPLICATION NUMBER: US 09/030,607
PRIOR FILING DATE: 1998-02-25
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 701
SOFTWARE: Paedseq for Windows Version 3.0
SEQ ID NO 536
LENGTH: 6140
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(6140)
OTHER INFORMATION: n=A,T,C or G
US-11-234-786-536

Alignment Scores:
Pred. No.: 0 Length: 6140
Score: 5600.50 Matches: 1300
Percent Similarity: 97.04 Conservative: 0
Best Local Similarity: 97.04 Mismatches: 0
Query Match: 97.34 Indels: 40
DB: 12 Gaps: 1

US-09-976-858-42 (1-1325) x US-11-234-786-536 (1-6140)
QY 26 TTPLeuAenProLeuPheLysIleGIYhISySaTgAgLeuGIuAaSPaSPheTYr 45
DB 225 TGGCTCAATCCCTTGTAAATGGCCATAACGAGATGAGAGATGATATGAT 294
QY 46 SerValIleuProGIuAaSPaSPheSerGIhISleuGIYGIuGIuLeuGIleGIYhISleuThrArgAlaIleIle 65
DB 295 TCAAGTGTGCGCAGAGACCGCTCACAGCCTTGGAGAGAGATGCGAAGGTTCTGGGAT 354
QY 66 LysGIuValIleuAArgAlaGIuAaSPaSPaGIuLysProSerLeuThrArgAlaIleIle 85
DB 355 AAAAGAGTTTAAAGCTGAGATGACGACAGAGCCTTCTTAAACAAGACATCATCA 414
QY 86 LysGySTYrTPPLySerTYrLeuValLeuGIYIlePheThrLeuIleGIuGIuSerAla 105
DB 415 AAGGTCTACTGGAATCTTATTAGTTTGGGAATTTTACCTTAATGAGAGAAAGTGCC 474

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QY 126 MetAaSPaSPaValAlaLeuAaSPaSPaThrAlaTYrAlaTYrAlaThrValIleuThrPheCysThr 145
DB 535 ATGATTCCTGTGGCTTTGAACACAGCGATGACCGCTGACCGGTCTGTTGGACG 594
QY 146 LeuIleLeuAlaIleLeuHISleIleuTYrPheTYrHISValGIuGIuAaGIYhISleArg 165
DB 595 CTCATTTGGCTATACCTCATCATCTTAATATTTTATACAGTTCAGTGTGCGGATGAG 654
QY 166 LeuAArgValAlaMetCysHISMetIleTYrArgValAlaLeuAArgLeuSerAaSPaAla 185
DB 655 TTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 714
QY 186 MetGIYhISleThrThrGIYGIuIleValAaSPaSPaSPaSPaSPaSPaSPaSPaSPa 205
DB 715 ATGGGAGAGACACACAGCGCAGATGATGATGATGATGATGATGATGATGATGATGAT 774
QY 206 AaSPaSPaValIlePheLeuHISleIleuThrAlaGIYProLeuGIuAlaIleAlaVal 225
DB 775 GATCAGGTGACAGTGTGTCTTACATCTGTGTGACAGACCATGACAGCATGACAGT 834
QY 226 ThrAlaLeuLeuThrMetGIuIleGIYIleSerCysLeuAlaGIYMetAlaValIle 245
DB 835 ACTGCCCTACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 894
QY 246 IleLeuLeuProLeuGIuIleSerCysPheGIYhISleuPheSerSerLeuAArgSerTYr 265
DB 895 ATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 954
QY 266 AlaThrPheThrAaSPaSPaAlaArgIleArgThrMetAaSPaSPaValIleThrGIYIleArgIle 285
DB 955, GCACCTTTCAGGAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 1014
QY 286 IleLysMetTYrAlaTrpGIuLysSerPheSerAaSPaSPaIleThrAaSPaSPaVal 305
DB 1015 ATAAATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1074
QY 306 GIuIleSerTYrIleLeuAArgSerSerCysLeuAArgIYMetAaSPaSPaSPaPhe 325
DB 1075 GAGATTTCAAGATTTCTGAAGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1134
QY 326 SerAlaSerTYrIleIleValIlePheValIleThrPheThrTYrTYrValIleuLeuGIYSerVal 345
DB 1135 AGTGCAGCAAAATCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1194
QY 346 IleThrAlaSerArgValIleValAlaValIleThrLeuTYrGIYAlaValArgLeuThrVal 365
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DB 1255 ACCCTCTTCTCCCTGACCATGAGAGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1314
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QY 406 GIYhISleYMetValIleValAlaIlePheThrAlaPheThrAaSPaSPaSPaSPaSPa 425
DB 1375 GGTAAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1434
QY 426 ProThrLeuGIuGIYLeuSerPheThrValArgProGIYGIuLeuLeuAlaValGIY 445
DB 1435 CCAACTTACAAAGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1494
QY 446 ProValGIYAlaGIYhISleSerSerLeuLeuSerAlaValIleuGIYGIuLeuAlaProSer 465
DB 1495 CCGGTGGAGAGAGAGATCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1554
QY 466 HISGIYLeuValSerValIleGIYArgIleAlaTYrValSerGIuGIuProThrValPhe 485

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Db 1555 CACGGGCTGCTCAGGCTGATGGAAGAAATTCCTATGTCCTCAGACAGCCCTGGGCTGTTCC 1614  
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 Db 1615 TCGGGAACCTCTGAGAGGATATATTTATTTGGGAAAGAAATACGAAAGGAACGATATGAA 1674  
 QY 506 LysValIleLysAlaCysAlaLeuLysLysAspLeuGlnLeuLeuGluAspGlyAspLeu 525  
 Db 1675 AAAGCATPAAAGGCTTGTCCTCTGAAAAAGATTTACAGCTGTGGAGGATGGTATCTCG 1734  
 QY 526 ThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGlnLysAlaArgValAsnLeu 545  
 Db 1735 ACTGTGAATAGAGATCGGGGAAACACGCTGAGTGGAGGGGCAAGAACCGGGTAAACCTT 1794  
 QY 546 AlaArgAlaValTyrGluAspAlaAspIleTyrLeuLeuAspAspProLeuSerAlaVal 565  
 Db 1795 GCAAGAGCATGTATCAAGATGCTGACATCTATCTCTGGACGATCTCTCAGTGCAGTA 1854  
 QY 566 AspAlaGluValSerArgHisLeuPheGluLeuCysIleCysGlnIleLeuHisGluLys 585  
 Db 1855 GATCGGGAAGTAGACAGACACTGTTCGAACTGTGATTTGTCAATTTTTCATGAGAAAG 1914  
 QY 586 IleThrIleLeuValIleThiIleGlnLeuGlnTyrLeuLysAlaAspSerGlnIleLeuIle 605  
 Db 1915 ATCACAAATTTTAGTACATCATCAGTTCAGTACCTCAAGCTGCAAGCTCAGATTCGATA 1974  
 QY 606 LeuLysAspGlyLysMetValGlnLysGlyThrTyrThrGluPheLeuLysSerGlyIle 625  
 Db 1975 TTGAAGATGTGTAAGATGTGCAAGAGGGGACTTACACTGAGTTCTTAAATCTGGTATA 2034  
 QY 626 AspPheGlySerLeuLeuLysLysAspAsnGluGlnSerGluGlnProValProGly 645  
 Db 2035 GATTTTGGCTCCCTTTTAAAGAGATATAGAAAGTAAACAACCTCCAGTTCAGGA 2094  
 QY 646 ThrProThrLeuArgAsnArgThrPheSerGluSerSerValITPserGlnIleSerSer 665  
 Db 2095 ACTCCACACTAAGGATGCTACTCTCAGAGCTTCGGTTCGCTCAACAACCTTCT 2154  
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 Db 2455 GGAATTTATTCAGGTTTAACTGATCTACCGTTCCTTTTGGCATAGCAAGATCTCTATGG 2514  
 QY 786 ValPheTyrValLeuValAsnSerSerGlnThrLeuHisAsnLysMetPheGluSerIle 805  
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Db 2635 TCAAAAGCATTTGACACTTGATGATGATTTGCTGCCCTGACGTTTTCATTAATTCAG 2694  
 QY 846 ThrLeuGlnValIleGlyValIleValSerValAlaValAlaValIleProThrIleAla 865  
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 QY 1126 LeuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGlnHisThrAspGluGlu 1145  
 Db 3535 TTGTTCACTGGAAACATAGAGAAACCTGGATCCCTTTAATGACACACGGATAGAGAA 3594  
 QY 1146 LeuTPAsnAlaLeuGlnGluValGlnLeuLysGluThrIleGluAspLeuProGlyLys 1165  
 Db 3595 CTGTGGAATGCTTTCAAGAGGTACAACTTAAAGAAACATTTGAAGATCTTCTGTGTA 3654  
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 DB 3775 AATGCGATCCAGAACTGATGATTATACAAAAAATCCGGAGAAATTTGCCAC 3834  
 QY 1226 CysThrValIleuThrIleAlaHisArgLeuAsnThrIleIleAspSerAspIleMet 1245  
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 QY 1266 GluSerLeuPheTyrIleMetValGlnIleuGluValAlaGluAlaIleIleuThr 1285  
 DB 3955 GAGAGCTATTTTACAAAGTGTGCAACAATCGGCGAAGCGCAAGCCCTGCTCACT 4014  
 QY 1286 GluThrAlaIleValGln----- 1290  
 DB 4015 GAAACAGCAAAACAGAGATGGGGTTTCAACATGTTGGCAAGCTGGTCAAACTCTGA 4074  
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 DB 4075 CCTCAAGTATCCACTGCTTGCCCTCCCAAACTGCTGAGATTACAGGTGTGAGCCACC 4134  
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 DB 4135 ACGCCAGCGCTGATGATCTTCAAAAGAAATTTATCCATATTTGGTCACACTGACCAACT 4194  
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 RESULT 6  
 US-11-124-367A-150  
 ; Sequence 150, Application US/11124367A  
 ; Publication No. US20060024700A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Michele Cargill  
 ; APPLICANT: Hongjin Huang  
 ; TITLE OF INVENTION: Genetic Polymorphisms Associated with  
 ; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof  
 ; FILE REFERENCE: CLO01519.ORD  
 ; CURRENT APPLICATION NUMBER: US/11/124,367A  
 ; CURRENT FILING DATE: 2005-05-09  
 ; PRIOR APPLICATION NUMBER: US 60/568,846  
 ; PRIOR FILING DATE: 2004-05-07  
 ; PRIOR APPLICATION NUMBER: US 60/582,609  
 ; PRIOR FILING DATE: 2004-06-25  
 ; PRIOR APPLICATION NUMBER: US 60/599,554  
 ; PRIOR FILING DATE: 2004-08-09  
 ; NUMBER OF SEQ ID NOS: 34460  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 150  
 ; LENGTH: 2143  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapiens  
 US-11-124-367A-150  
 Alignment Scores:  
 Pred. No.: 1,056-308 Length: 2143  
 Score: 3110.50 Matches: 656  
 Percent Similarity: 92.8% Conservative: 0  
 Best Local Similarity: 92.8% Mismatches: 0  
 Query Match: 48.8% Indels: 51  
 DB: 12 Gaps: 1  
 US-09-976-858-42 (1-1325) x US-11-124-367A-150 (1-2143)  
 QY 1 NetLeuProValIleGlnIleValIlePheAsnProLeuGlnAspAlaAsnLeuCysSer 20  
 DB 22 ATGTCGCCGCTGTACAGAGAGGTGAAGCCCAACCCGCTGACAGACCGCAACCTCTGCTCA 81

QY 21 ArgValPhePheTrp----- 25  
 DB 82 CGCGTCTTCTTGCTGCTCCGCCGCTCTTTTGGAAAGACACTTGCATTGATTGATAG 141  
 QY 25 ----- 25  
 DB 142 GACCCACTTGATTAATCCAGATGATGCTTCACTCAACATCTCAGTTTAATTCAG 201  
 QY 26 -----TyrLeuAsnPro 29  
 DB 202 TGCAAATACCTTTTCCCAATTAACATTCATTCTTACAGAAAGTGGCTCAATCCC 261  
 QY 30 LeuPheValIleGluHisIleValArgArgLeuGluGluAspAspMetTyrSerValIlePro 49  
 DB 262 TTTGTTAAATTTGGCATTAACGAGATTAGAGAAATGATATGATATTCAGTGGTCCA 321  
 QY 50 GluAspArgSerGlnHisIleuGluValGluValPheTyrAspIleValIleu 69  
 DB 322 GAAAGACCCCTCACACACCTTGAGAGAGGTTGCAAGGGTCTGGGATTAAGAGTTTAA 381  
 QY 70 ArgAlaGluAsnAspAlaGluIleProSerLeuThrArgAlaIleIleValCysTyrTrp 89  
 DB 382 AGAGCTGAAATGACGACAGAAAGCTTTTAAACAAGCAATCAATAAAGTTACTCG 441  
 QY 90 LysSerTyrLeuValIleuGluYIlePheThrIleuIleGluIleSerAlaValIleGln 109  
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 QY 110 ProIlePheLeuGluValIleAsnTyrPheGluAsnTyrAspProMetAspSerVal 129  
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 QY 130 AlaLeuAsnThrAlaIleTyrAlaIleThrValIleuThrPheCysThrIleuIleuAla 149  
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 QY 190 ThrThrGluGlnIleValAsnLeuLeuSerAsnAspValAsnIlePheAspGlnValThr 209  
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 DB 1102 ATTCAGAAAGTTCTGCTCAGAGAGATGAAATTTGCTCATTTTTCAGTCCAAAGCAAA 1161  
 QY 330 IleIleValPheValThrPheThrThrValIleuLeuGluYsSerValIleThrAlaSer 349

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Db      1162 ATCATGCTGTTGTGACCTTCAACCACTACGCTGCTCCGGAAGTGATCAAGCAAGC 1221
Qy      350 ArgValAlpheValAlValAlThrLeuYrGlyAlaValArgLeuThrValAlThrLeuPhePhe 369
Db      1222 CCGGCTTCCTGCTGAGCTGATGAGGCTGTGCGGCTGAGGCTTACCTCTTCTTC 1281
Qy      370 ProSerAlaIleGluValArgValSerGluAlaIleValSerIleArgArgIleGlnThrPhe 389
Db      1282 CCTCAGCATTGAGAGGGGTGTCAAGGGCAATGTCAGCATCCGAAGATCCAGACCTTT 1341
Qy      390 LeuLeuLeuAspGluIleSerGlnArgAlaArgGlnLeuProSerAspGlyIleValMet 409
Db      1342 TTGCTACTTGATGAGATATCAAGGCCAACCGTCAGCTCCGTCAGATGTTAAAGAAAG 1401
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Qy      430 GlyLeuSerPheThrValArgProGlyGluLeuLeuAlaValGlyProValGlyAla 449
Db      1462 GGCCTTTCTTACTGTCAAGCCTGGCGAATTTGTAGCTGTGGTGGCCCGTGGGAGCA 1521
Qy      450 GlyIleSerSerLeuLeuSerAlaValLeuGlyGluLeuAlaProSerHisGlyIleVal 469
Db      1522 GGGAAAGTCATCACTGTTAAGTCCGTCGCGGGAATTTGGCCCAAGTCACGCGCTGCTC 1581
Qy      470 SerValHisGlyArgIleAlaTyrValSerGlnGlnProTyrValPheSerGlyThrLeu 489
Db      1582 ACGCTGCATGAAAGATTCCTATGTGTCTCAGCAAGCCCTGGGTGTTCTCGGGAACCTCTG 1641
Qy      490 ArgSerAsnIleLeuPheGlyIleValYrGlyIleValYrGlyIleValYrGlyIleValYr 509
Db      1642 AGAGATTAATATTATTATTTGGAGAAATAAGAAAGAAAGCAATATGAAAGATCAATTAAG 1701
Qy      510 AlaCyAlaIleuValYrLeuGlnLeuLeuGlnLeuLeuGlnLeuLeuGlnLeuLeuGln 529
Db      1702 GCTTGGCTCTGAAAGAAAGATTTTACGCTGTGAGAGATGTGATCTGATGATAGCA 1761
Qy      530 AspArgGlyIleThrThrLeuSerGlyGlyGlnYrAlaArgValAsnLeuAlaArgAlaVal 549
Db      1762 GATCGGGAAACCAAGCTGATGAGAGGCGAAGAAAGCAAGGATTAACCTTCAGAGAGCAAG 1821
Qy      550 TyrGlnAspAlaAspIleTyrLeuLeuAspAspProLeuSerAlaValAspAlaGluVal 569
Db      1822 TATCAAGATGCTGACATCTATCTCTCGAGCAATCTCTCAGTCAGTATGAGTGGAAAGTT 1881
Qy      570 SerArgHisLeuPheGluLeuGlyIleGlyGlnIleLeuHisGlyIleValIleThrIleLeu 589
Db      1882 ACGACGACCTTGTTCGACACTGTGATTTGTCAAAATTTTCATGAGAAAGATCAACAATTTTA 1941
Qy      590 ValThrHisGlnLeuGlnTyrLeuYrAlaIleAspGlnIleLeuIleLeuYrAspGly 609
Db      1942 GTGACTCATCACTGTCAGTACCTCCAAAGCTGCAAGTCAAGTTCGATATTTGAAAGATGT 2001
Qy      610 LysMetValGlnIleGlyIleThrYrThrGlnPheLeuYrSerGlyIleAspPheGlySer 629
Db      2002 AAAATGTGTCAAGAAAGGGAATTACACTGAGTTCTTAAATCTGGTATTAATTTTGGCTCC 2061
Qy      630 LeuLeuYrLeuYrAspAsnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 649
Db      2062 CTTTTTAAAGAGATATATGAGAAAGTGAACAACCTCAGTTCAGAACTCCACACATA 2121
Qy      650 ArgAsnArgThrPheSerGlu 656
Db      2122 AGGAATCGTACTTCTCAAGG 2142

```

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; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; FILE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 148
; LENGTH: 2256
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-124-367A-148

Alignment Scores:
Pred. No.: 5,42e-304 Length: 2256
Score: 3262.00 Matches: 655
Percent Similarity: 87.9% Conservative: 0
Best Local Similarity: 87.9% Mismatches: 1
Query Match: 48.1% Indels: 90
DB: 12 Gaps: 1

US-09-976-858-42 (1-1325) x US-11-124-367A-148 (1-2256)
Qy      1 MetLeuProValTyrGlnGluValYrProAsnProLeuGlnAspAlaAsnLeuCySer 20
Db      22 ATGCGCCCGTGTACAGAGAGGTGAAGCCCAACCGCTGCAAGAGCGAAGCCTGTCTCA 81
Qy      21 ArgValAlphePheTrp----- 25
Db      82 CCGGCTTCCTTCTG-ATGAGATCTGCTGTGTACCCAGCTGAGTGCAGTGGCCACT 140
Qy      25 ----- 25
Db      141 CTCAGCTCAGTCAGACCTCACTCTCTGTTCAAGAGATCCTCTGCTCAGCACCAG 200
Qy      25 ----- 25
Db      201 ACTAGCAGGTCTCCCGCTCTTCTTCTTGAAGACACTTGCATTGATTTAGACCA 260
Qy      25 ----- 25
Db      261 CTGGATTAATCCAGATGATGTCTTCACTCCAACTCTCACTTTAATTCATGTCAAA 320
Qy      26 -----TriLeuAsnProLeuPhe 31
Db      321 TACCTTTTCCAAATAACATTCAATCTTTTACAGAGAAAGGTGCTCAATCCCTGTTT 380
Qy      32 LysIleGlyHisIleValArgArgLeuGlnGlnAspAspMetTyrSerValLeuProGluPhe 51
Db      381 AAAATTTGGCATTAACGAGATTTAGAGAAAGTATGATATCTAGTGTGCAAGAGC 440
Qy      52 ArgSerGlnHisLeuGlyGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 71
Db      441 CGCTCAGCAGCCTTGGAGAGAGGTGCAAGGGTCTGGGATTAAGAAAGCTTTTAAAGAGCT 500
Qy      72 GluAsnAspAlaGlnIleYrProSerLeuThrArgAlaIleIleLysCySerTyrTrpLysSer 91
Db      501 GAGATGACGACAGAGAGCTCTTTTAAACAAGCATATTAAGTGTACTGAAATCT 560
Qy      92 TyrLeuValLeuGlyIlePheThrLeuIleGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 111
Db      561 TATTTAGTTTGGAGATTTTACGTAAATTGAGAAAGTCCAAAGTATTCAGGCCATA 620
Qy      112 PheLeuGlyIleIleIleAsnTyrPheGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 131
Db      621 TTTTGGGAAAAATTAATTAATTTTGAATAATTAAGATCCATGAGATTCGTGGCTTGG 680

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QY 132 AenthrAlaTyrAlaTyrAlaThrValLeuThrPheCysThrLeuIleuAlaIleu 151  
 Db 681 AACACAGCGTACGCTATGCAAGCGTGTGACCTTTTGACCGCTCATTTGGCTACAG 740  
 QY 152 HisH1sLeuTyrPheTyrHisValGlnCysAlaGlyMetArgLeuArgValAlaMetCys 171  
 Db 741 CATCATATATATTTTATCATCGTTACGTGTGCTGGATGAGGTATGAGATACCATGTC 800  
 QY 172 HisMetIleTyrArgValAlaLeuArgLeuSerAspMetAlaMetGlyTyrThrThr 191  
 Db 801 CATATGATTTATCGGAAGCGACCTGCTTATGATCATGCGCATGGGGAAGCAACACA 860  
 QY 192 GlyGlnIleValAsnLeuSerAspValAsnLeuPheAspGlnValThrValPhe 211  
 Db 861 GGCCAGATATGCAATCTGCTGTCATATGATGATGAAACAAATTTGATCAGGATGTC 920  
 QY 212 LeuHisPheLeuThrAlaGlyProLeuGlnAlaIleValThrAlaLeuLeuThrPhe 231  
 Db 921 TTACACTTCTGTGGCAGAGACCATGCAAGCGATTCGATGCTGCTGATG 980  
 QY 232 GlnIleGlyIleSerCysLeuAlaGlyMetAlaValLeuIleIleLeuLeuProLeuGln 251  
 Db 981 GAGATAGGAATATCGTGTGCTGCTGCGATGCGAGTTCTATCATCTCTGCGCTTGCAA 1040  
 QY 252 SerCysPheGlyIleLeuLeuPheSerLeuArgSerIleThrAlaThrPheThrAla 271  
 Db 1041 AGCTGTTTGGAGAGTTGTTCTATCATCAGAGAGTAAACAGCACTTTCAGAGATGCG 1100  
 QY 272 ArgIleArgThrMetAsnGlnValIleThrGlyIleArgIleIleLeuMetTyrAlaThr 291  
 Db 1101 AGGATCAGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1160  
 QY 292 GlnIleSerPheSerAsnLeuIleThrAsnLeuArgValGlyGlnIleSerIleLeu 311  
 Db 1161 GAAAGTCACTTTTCAATCTTATTTACCAATTTGAGAAAGAGATTTCCAAAGATTCG 1220  
 QY 312 ArgSerSerCysLeuArgIleMetAsnLeuAlaSerPhePheSerAlaSerIleIle 331  
 Db 1221 AAGAGTCTGCTGCTCAGAGGATGAAATTTGGCTTCAATTTTTCAGAGCAAAATCAGC 1280  
 QY 332 ValPheValThrPheThrThrTyrValLeuLeuGlnSerValIleThrAlaSerArgVal 351  
 Db 1281 GTGTTTGTACCTTCCACCACTTACGTCCTCTCGGAGTGTATTCACAGCCGCGCG 1340  
 QY 352 PheValAlaValThrLeuTyrGlyAlaValArgLeuThrValThrLeuPhePheProSer 371  
 Db 1341 TTCGTGGCAGTGAACGCTGATGCGGCTGCGGCTGACGTTACCTTTCCCTCA 1400  
 QY 372 AlaIleGlnArgValSerGlnAlaIleValSerIleArgArgIleGlnThrPheLeuLeu 391  
 Db 1401 GCCATTGAGAGGATGTCAGAGCAATTCGACATTCGAGATTCGAGATTCGAGATTCG 1460  
 QY 392 LeuAspGlnIleSerGlnArgAsnArgGlnLeuProSerAspGlyValAlaMetValHis 411  
 Db 1461 CTTGATGAGATTCACAGCGCAACCTTCAGCTGCTCGATGATGATGATGATGATGATG 1520  
 QY 412 ValGlnAspPheThrAlaPheThrAspValAspSerIleThrProThrLeuGlnIleLeu 431  
 Db 1521 GTGCAAGATTTTACGCTTTTGGGATAGGATCAGAACCCCAACTTCAAGGCTT 1580  
 QY 432 SerPheThrValArgProGlyIleLeuLeuAlaValAlaGlyProValGlyAlaGlyLys 451  
 Db 1581 TCCCTTATCGTCAAGCTGCGCAATTTGATGCTGTGTGCGGCCCTGCGAGACAGGAG 1640  
 QY 452 SerSerLeuLeuSerAlaValLeuGlyIleLeuAlaProSerHisGlyLeuValSerVal 471  
 Db 1641 TATCATCTTTATGAGCGCTGCTCGGAGATTTGCCCCCAAGTACCGGCTGTACCGTG 1700  
 QY 472 HisGlyArgIleAlaTyrValSerGlnGlnProThrValPheSerGlyThrLeuArgSer 491  
 Db 1701 CATGGAAGATTTGCTATGATGCTCAGACGCGCTGCTGTCTCGGGAACCTGAGAGAT 1760

QY 492 AsnIleLeuPheGlyIleValSerTyrGlnIleValArgIleValValIleValAlaCys 511  
 Db 1761 AATATTTATTTGGAGAAATATACAAAAGAACATATGAAAAGTCAATAAGCTTGT 1820  
 QY 512 AlaLeuIleValAspLeuGlnLeuLeuGlnAspGlyAspLeuThrValIleGlyAspArg 531  
 Db 1821 GCTCGAAAAGATTTACAGCTGTGGAGATGATGATGATGATGATGATGATGATGATG 1880  
 QY 532 GlyThrThrLeuSerGlyGlnIleValArgValAsnLeuAlaArgAlaValIleGln 551  
 Db 1881 GGAAACAGCTGAGTGGAGGCGAAGAACACGGTAACTTTGCAAGAGCAGTATCA 1940  
 QY 552 AspAlaAspIleTyrLeuLeuAspAspProLeuSerAlaValAlaAspAlaGlyValSerArg 571  
 Db 1941 GATGCTGACATCTATCTCTGACATCTCTCTCATGCAATGATGCGGAATTTGACGA 2000  
 QY 572 HisLeuPheGlnLeuCysIleCysGlnIleLeuHisGlyIleThrIleLeuValThr 591  
 Db 2001 CACTTGTTCGAACCTGTATTTGTCAATTTTGCATGAGAAATCAACAATTTTATGACT 2060  
 QY 592 HisGlnLeuGlnTyrLeuLeuAlaAlaSerGlnIleLeuIleLeuValAspGlySerMet 611  
 Db 2061 CATCAGTTCAGTACCTTCAAGCTGCAAGTCAAGATTCGATGATGATGATGATGATG 2120  
 QY 612 ValGlnIleGlyThrTyrThrGlnPheLeuIleAspSerGlyIleAspPheGlySerLeu 631  
 Db 2121 GTGCAAGGAGGACCTTACATGAGTCTTAAATTTGATGATGATGATGATGATGATG 2180  
 QY 632 LysIleAspAsnGlnIleSerGlnIleProValProGlyThrProThrLeuArgAsn 651  
 Db 2181 AAGAGATATATGAGAAAGGAAAGCAACCTCAGTTCCAGGAATCCCACTAAGAAAT 2240  
 QY 652 ArgThrPheSerGln 656  
 Db 2241 GTTACCTTCTCAGAG 2255

## RESULT 8

US-10-826-585-35  
 ; Sequence 35, Application US/10826585  
 ; Publication No. US2006008807A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Immunivest Corporation  
 ; APPLICANT: O'Hara, Shawn Mark  
 ; APPLICANT: Foulik, Brad  
 ; APPLICANT: Zweitzig, Daniel  
 ; TITLE OF INVENTION: Multiparameter analysis of comprehensive nucleic acids and  
 ; FILE REFERENCE: IMNC 143 PCT/US  
 ; CURRENT APPLICATION NUMBER: US/10/826,585  
 ; CURRENT FILING DATE: 2004-04-16  
 ; PRIOR APPLICATION NUMBER: 60/369945  
 ; PRIOR FILING DATE: 2002-04-04  
 ; PRIOR APPLICATION NUMBER: 60/330669  
 ; PRIOR FILING DATE: 2002-11-26  
 ; PRIOR APPLICATION NUMBER: PCT/US02/26867  
 ; PRIOR FILING DATE: 2002-08-23  
 ; NUMBER OF SEQ ID NOS: 131  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 35  
 ; LENGTH: 5011  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-10-826-585-35

## Alignment Scores:

Pred. No.:	2,816-209	Length:	5011
Score:	2285.50	Matches:	528
Percent Similarity:	56.6%	Conservative:	274
Best Local Similarity:	37.3%	Mismatches:	491
Query Match:	33.7%	Indels:	124
DB:	7	Gaps:	30

US-09-976-858-42 (1-1325) x US-10-826-585-35 (1-5011)



Db 2900 GTGACGACAGTGCAGGAGGAACTGCAGACAGCTCAGGAGCTCTCTCTCAATAGT 2959  
 Qy 662 GINGInserSerArgProserleuYbaBglYAlaLeuGInserGInserThrGluAn 681  
 Db 2960 GGGGACATCAAGGACCAACAGACCGGAGAACTGAGAAAGTGAAGCCAGCAAG 3019  
 Qy 682 ValProVal---ThreuserGluGluAenArgserGlu---GlyValGlyPheGln 699  
 Db 3020 GAGGAGACCTGGAAGTGAATGAGGCTGACAGGCCACAGAGGAGGTCAAGCTTCC 3079  
 Qy 700 AlaTyrLysAsnTyrPheArgAlaGlyAlaHisStrpIleValPhe-----IlePheLeu 717  
 Db 3080 GGTGACTGGGACTACATGAAGGCATCGGACTCTTCATCTCTCTCTCAGACATCTTCC 3139  
 Qy 718 IleLeuLeuAsnThrAlaAlaGlnAlaAlaTyrValLeuGlnAspTrpTrpLeuSerTyr 737  
 Db 3140 TTCATGTGTGAC-----CATGTGTCCGGCTGGCTTCACAACTATTGGCTCAGCCCTC 3190  
 Qy 728 TrpAlaAsnLysGInserMetLeuAsnValThrValAsnGlyGlyValAsnValThrGlu 757  
 Db 3191 TGGAGCTGAT-----GACCCCATCTGACAGGAGCTCAGAGACAGCAAGAA 3235  
 Qy 758 ---LysLeuAspLeuAsnTrpTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrVal 776  
 Db 3236 GTCCGGCTGAGGCTCATGAGAGCCCTGGGCAATTTCACAGGAGATGCGCTG----- 3286  
 Qy 777 LeuPheGlyIleAlaArgSerLeuLeuValPheTyrValLeuValAsnSerGlnThr 796  
 Db 3287 ---TTTGGTACTCTCCATTCGCTTCATCGGGGGGATCTTG-----GCTTCCGCTCT 3337  
 Qy 797 LeuHisAsnLysMetPheGluSerIleLeuLysAlaProValLeuPhePheAspArgAn 816  
 Db 3338 CTGACAGTGGAGCTGTGCACAGACATCTGCGGTCAACCAAGAGCTCTTTCAGGGAGCC 3397  
 Qy 817 ProIleGlyArgIleLeuAsnArgPheSerLysAspIleGlyHisLeuAspAspLeu 836  
 Db 3398 CCCAGTGGAGACCTGGTGAACGGCTTCTCCAGAGAGCTGAGACAGTGAATCCATGATC 3457  
 Qy 837 ProLeuThrPheLeuAspPheIleGlnThrLeuLeuGlnValValGlyValValSerVal 856  
 Db 3458 CCGGAGGTCATCAAGATGTTCAAGGCTCCCTGTTCAACGTCATGTCCTCTCATCTGTT 3517  
 Qy 857 AlaValAlaValIleProTrpIleAlaIleProLeuValProLeuGlyIleIlePheIle 876  
 Db 3518 ATCTGTGGCCACCGCCATCCGCGGCATCATCATCCGCCCTTGGCTCATCTAATCCTC 3577  
 Qy 877 PheLeuArgTyrPheLeuGluThrSerArgAspValLysArgLeuGlnSerThrThr 896  
 Db 3578 TTCGTCAGAGGTTCTACGCTGCTCTCCCGAGCTAGAGGCTCCAGTCCGCTCAGC 3637  
 Qy 897 ArgSerProValPheSerHisLeuSerSerLeuGlnGlyLeuTrpThrIleArgAla 916  
 Db 3638 CCTCCCGCGGTCTATCCCATTTCAACGAGACCTTCTGCGGGGTCAAGCTCATTTGAGCC 3697  
 Qy 917 TyrLysAlaGlnGluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGlu 936  
 Db 3698 TTCGAGGACAGAGAGGCTTCATCCACAGAGTACCTGAGGTGACAGAGCAAGCAAG 3757  
 Qy 937 AlaTrpPheLeuPheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCys 956  
 Db 3758 GCTTATATCCCAAGCATCTGTGCGCAACAGGTGCTGCGCTGCGGTGAGTGTGGGC 3817  
 Qy 957 AlamePheValIleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAla 976  
 Db 3818 AACTGCATGCTTCTGTTGCTGCTGCTTGGGTGATCTCCAGGACAGAGCCATGCT 3877  
 Qy 977 GlyGlnValGlyLeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPheGlnTrpCys 996  
 Db 3878 GCGTGGTGGGCTCTCAAGTGTCTTACTATTCAGAGTCAACAGTACTGAACTGGCTG 3937  
 Qy 997 ValArgGlnSerAlaGluValGluAsnMetIleSerValGluArgValIleGluTyr 1016

Db 3938 GTTCGATGTCATCTGAATGAGAAACCAACATCGTGGCCGTGGAGAGGCTCAAGAGTAT 3997  
 Qy 1017 ThrAspLeuGluLysGluAlaProTrpGluTyrGlnLys---ArgProProValTrp 1035  
 Db 3998 TCAGAGACTGAGAGAGAGGCGCCCTGGCAATTCAGAGAGACAGCTCCGCCAGAGCTGG 4057  
 Qy 1036 ProHisGluGlyValIleIlePheAspAsnValAsnPheMetTyrSerProGlyPro 1055  
 Db 4058 CCCGAGGTGGGCGGAGTGAATTCGGAATCTACTGCTCGGCTACCGAGAGAGACTGGAC 4117  
 Qy 1056 LeuValLeuLysHisLeuThrAlaLeuIleLysSerGlnGluValGlyIleValGly 1075  
 Db 4118 TTCGTTCTCAGGACATCAATGTCAGATCAATGAGGAGAAAGGTGGCATCGTGGG 4177  
 Qy 1076 ArgThrGlyAlaGlyLysSerSerLeuIleSerAlaLeuPheArgLeuSerGlu---Pro 1094  
 Db 4178 CGAGCGGAGGCTGGAGAGTCTCTCTGACCTCGGCTTATTTCCGATACAGAGCTTCC 4237  
 Qy 1095 GlnGlyLysIleTrpIleAspLysIleLeuThrThrGluIleGlyLeuHisAspLeuArg 1114  
 Db 4238 GAGGAGAGATCATCATGATGAGATCAACATCCGCAAGATCGGCTCAGACACTCCGC 4297  
 Qy 1115 LysLysMetSerIleIleProGlnGluProValLeuPheThrGlyThrMetArgLysAn 1134  
 Db 4298 TTCAGATCACCATCATCTCCGAGGACCTGTGTTGTTTGGGGTTCCTCCGATGAC 4357  
 Qy 1135 LeuAspProPheAsnGluHisThrAspGluGluLeuThrPanAlaLeuGlnGluValGln 1154  
 Db 4358 CTGACCCATTCAGCACTACTCGGATGAGAAAGTGAAGTCAAGTCTCTGAGCTGGCCAC 4417  
 Qy 1155 LeuLysGluThrIleGluAspLeuProGlyLysMetAspTrpGluLeuAlaGlnSerGly 1174  
 Db 4418 CTGAAGACTTCGTCTGACCCCTTCTCTGACAGCTAGACATGATGTCAGAAAGCGGG 4477  
 Qy 1175 SerAsnPheSerValGlyGlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLys 1194  
 Db 4478 GAGAACTCAAGTGTGGGACAGCGCACTTGTGTGCTTACGAGCCGGGCTCTGAGGAG 4537  
 Qy 1195 AsnGlnIleLeuIleIleAspGluAlaThrAlaAsnValAspProArgThrAspGluLeu 1214  
 Db 4538 AGCAAGATCTTGTGTGATGAGGCAACGCGACCGTGGACCTGGAACCGAGCACTC 4597  
 Qy 1215 IleGlnLysLysIleArgGluLysPheAlaHisCysThrValLeuThrIleAlaHisArg 1234  
 Db 4598 ATCCAGTCCACCATCCGAGACACAGTTCAGAGACTGACCGTCTCAACATGCCACCG 4657  
 Qy 1235 LeuAsnThrIleIleAspSerAspLysIleMetValLeuAspSerGlyArgLeuLysGlu 1254  
 Db 4658 CTCAACACATCATGATGATCAACAGAGGTGATCGTTCGACAAAGAGAAATCAGAG 4717  
 Qy 1255 TyrAspGluProTyrValLeuLeuGlnAsnLysGlnSerLeuPheTyrLysMetValGln 1274  
 Db 4718 TACGCGGCCCATCGAGACTCTCTGACAGAGAG---GGTCTTTCTTACAGCATGCGCAA 4774  
 Qy 1275 GlnLeuGly-----LysAlaGlnAlaAlaIleLeuThrGluThrAlaLysGlnVal 1291  
 Db 4775 GAGCGCGCTGTGTGTGAGCCCGCAGAGCTGGCATCTCTGTCAGAACTGAGGCTTAT 4834  
 Qy 1292 Tyr-----PheLysArgAsnTyrProHisIleGlyHisThrAspHisMetValThr 1308  
 Db 4835 TGCCAGCGCCAGGAGAGAGTACAGTACCTCG--GTAACCAAGCTCCACACTGAAC 4893  
 Qy 1309 AsnThrSerAsnGlyLysProSerThrLeuThrIlePheGlnThrAla 1324  
 Db 4894 AAAACATAAAAACCAAAACCAAGACAAACCAAAACATATTCAAGAGCA 4941

## RESULT 9

US-11-045-578-3  
 ; Sequence 3, Application US/11045578  
 ; Publication No. US20060024685A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HO, Rodney J.Y.  
 ; APPLICANT: YANG, Ziping

```

APPLICANT: SHEN, Danny D.
APPLICANT: WU, Daniel
TITLE OF INVENTION: NOVEL SEQUENCE VARIANTS OF MULTI-DRUG RESISTANCE GENES, MDR1 AND
TITLE OF INVENTION: MRP1, AND RECOMBINANT CELLS EXPRESSING MRP1 AND MDR1 FOR
TITLE OF INVENTION: ASSESSMENT OF DRUG PENETRATION AND DISPOSITION
FILE REFERENCE: 016336-002510US
CURRENT APPLICATION NUMBER: US/11/045,578
PRIOR FILING DATE: 2005-01-26
PRIOR APPLICATION NUMBER: US 60/539,362
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.3
SEQ ID NO 3
LENGTH: 5011
TYPE: DNA
ORGANISM: human
US-11-045-578-3

Alignment Scores:
Pred. No.: 2,81e-209 Length: 5011
Score: 2285.50 Matches: 528
Percent Similarity: 56.6% Conservative: 274
Best Local Similarity: 37.3% Mismatches: 491
Query Match: 33.7% Indels: 124
DB: Gaps: 30

US-09-976-858-42 (1-1325) x US-11-045-578-3 (1-5011)
QY 3 ProValTYrGlnGluVal-----LYProAnProLeuGlnAsp-----AlaAsnLeu 18
DB 782 CCCGTTTCGGAACCATCCACGACCTTAATCCCTGCGCAGAGTCGACCGCTTCCTTC 841
QY 19 CysSerArgValPhePheTrpTrpLeuAsnProLeuPheValIleGlyHisArgArg 38
DB 842 CGTGCGAGATCACTTCGTGTCATCAAGAGTTATGTCGGGGCTACCGCCAGCC 901
QY 39 LeuGlnGluAspAspMetTyrSerValLeuProGluAspArgSerGlnHisLeuGln 58
DB 902 CTGAGGCGAGTGAACCTGTGCTTAAACAAGAGACACGTCGGACAAGTCGCT 961
QY 59 GluLeuGlnGlyPheTrpAspArgGlu----- 67
DB 962 GTTTTGTAAGAAGACTGGAAGAAATGCGCCAGACTAGAACGACCGGTGAAGTT 1021
QY 68 ValLeuArgAlaGluAsnAspAlaGln----- 76
DB 1022 GTGTACTCTCCAAAGATCTGCGCCAGCGAAAGAGTTCCAAAGTGAATGCAATG 1081
QY 77 -----LYProSerLeuThrArg 82
DB 1082 GAGGTGAGGCTTTGATCGTCAAGTCCCAAGAAAGAGTGAAGAGTGAAGTGAAGT 1141
QY 83 AlaIleIleLysCysTyrTrpLysSerTyrLeuValLeuGlyTyrPheThrLeuIleGlu 102
DB 1142 GTGTATACAAAGCCTTGGGCGCTTACTTCATAGCTTCTTCTTCAAGCCATCCAC 1201
QY 103 GluSerAlaLysValIleGlnProIlePheLeuGlyValIleAsnTyrPheGluAsn 122
DB 1202 GACCTGATGATGTTTCCGGGCGCGAGATCTTA--AAGTGTCTCACTCAAGTTCGTAAT 1258
QY 123 TyrAspProMetAspSerValAlaLeuAsnThrAlaTyrAlaTyrAlaThrValLeuThr 142
DB 1259 -----GACACGAAGCGCCCAAGCTGGCAGGCTTCTTCAACCGTGGCTG 1306
QY 143 PheCysThrLeuIleLeu---AlaIleLeuHisLeuTyrPheTyrHisValGlnCys 161
DB 1307 TTGTGACACCTGCTGCGAGACCTCGTGCACACAGTACTTCCACATCTGCTTCGTC 1366
QY 162 AlaGluMetArgLeuArgValAlaMetCysHisMetIleTyrArgValAlaLeuArgLeu 181
DB 1367 AGTGCGATGAGTCAAGACCGCTGTCAATTGGGGCTGTCTATCGAAGGCGCTGGTGAATC 1426
QY 182 SerAsnMetAlaMetGlyLysThrThrThrGlnIleValAsnLeuLeuSerAsnAsp 201

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DB 1427 ACCATTTCAGCAGAAAATCTCCACGCTCGGGAGATGTCACCTCATATCTGTGGAC 1486
QY 202 ValAsnLysPheAspGlnValThrValPheLeuHisPheLeuTrpAlaGlyProLeuGln 221
DB 1487 GCTAGAGGTTCAAGGACTTGGCCACGTCACATTAACATGATCTGTGACGCCCTCGCA 1546
QY 222 AlaIleAlaValThrAlaLeuLeuTrpMetGluIleGlyIleSerCysLeuAlaGlyMet 241
DB 1547 GTCACTCTGCTCTCACTCTGTCGTGAATGCGGCCCTCGCTCGCTGCTGGAAGTG 1606
QY 242 AlaValLeuIleIleLeuLeuProLeuGlnSerCysPheGlyLysLeuPheSerSerLeu 261
DB 1607 GCGGTGATGTCCTCATGTGTCCTGCAATGCTGTG-----ATG 1645
QY 262 ArgSerLysThrAlaThrPhe-----ThrAspAlaArgIleArg 274
DB 1646 GCGATGAAGACCAAGACCTATCAGGTGGCCCAATGAAGACCAAGACCAATCGATCAAG 1705
QY 275 ThrMetAsnGluValIleThrGlyIleArgIleIleLysMetTyrAlaTrpGluLysSer 294
DB 1706 CTGATGAACGAATTCATCATGGATCAAAAGTCTTAAGCTTATGCTGGGAGCTGGCA 1765
QY 295 PheSerAsnLeuIleThrAsnLeuArgLysGluIleSerLysIleLeuArgSerSer 314
DB 1766 TTCAGGACAAGAGTGTGCTGCATCAGCAGCAGAGAGCTGAAGGTCTGAAGAGCTGCGC 1825
QY 315 CysLeuArgGlyMetAsnLeuAlaSerPheSerAlaSerLysIleIleValPheVal 334
DB 1826 TACCTTGACCGCGTGGGACCTTCACTGAGTGTGCACGCCCTTCTGTGCTTCGTC 1885
QY 335 ThrPheThrThrTyrValLeuLeu-----GlySerValIleThrAlaSerArgValPhe 352
DB 1886 ACATTGCGCGTCAAGTACCATGACAGAAACAACATCTGATGCGCAGACAGCTTC 1945
QY 353 ValAlaValThrLeuTyrGlyAlaValArgLeuThrValThrLeuPhePheProSerAla 372
DB 1946 GTGTCTTGGGCTGTTCAACATCTCGGCTTCCCGTCGAACTT---CTCCCATGCTC 2002
QY 373 IleGluArgValSerGluAlaIleValSerIleArgArgIleGlnThrPheLeuLeu 392
DB 2003 ATCAGCAGACCTGTGACGAGCAAGTCTCTCCATCAACCCCTGAAGATTTTCTCTCCAT 2062
QY 393 AspGluIleSer-----GlnArgAsnArgIleuProSerAspGlyLysLys 408
DB 2063 GAGAGGCTGGAACCTGACAGATGAGCAGCGGCTGTCAAAAGCGCGGGGGACGAGAC 2122
QY 409 MetValHisValGlnAspPheThrAlaPheTrpAspLysAlaSerGluThrProThrLeu 428
DB 2123 AGCATCACCGTAGAGATGACACATTCACCTGGGCGAGG---AGGACCTCCACACCTG 2179
QY 429 GlnGlyLeuSerPheThrValArgProGlyIleLeuLeuAlaValIleGlyProValGly 448
DB 2180 AATGGCATCACCTTTCATCTCCAGAGGTCCTTGGTGGCGGTGTGGGCGAGGTGGG 2239
QY 449 AlaGlyLysSerSerLeuLeuSerAlaValIleGlyGluLeuAlaProSerHisGlyLeu 468
DB 2240 TGGCGAAAGTGTCTCTCTCAAGCTCTTGGTGTGAGTGAAGCAAGTGAAGGGGAC 2299
QY 469 ValSerValHisGlyArgIleAlaTyrValSerGlnGlnProTrpValPheSerGlyThr 488
DB 2300 GTGGCTATCAAGGGCTCGGTGCTATGTGCACAGCAGGCTGGATTCACAATATCTCT 2359
QY 489 LeuArgSerAsnIleLeuPheGlyLysLysTyrGlyLysGluArgTyrGlyValIle 508
DB 2360 CTCGAGAAAACATCTCTTTTGGAGTCAAGTGAAGCAACATATTAAGGTCCGTGATA 2419
QY 509 LysAlaCysAlaLeuLysLysAspLeuGlnLeuLeuGluAspGlyAspLeuThrValIle 528
DB 2420 CAGGCTGTGCTCTCTCCAGACCTGGAATCTGCCAATGGGAGTGGACAGAGTT 2479
QY 529 GlyAspArgGlyThrThrLeuSerGlyGlyGlnLysAlaArgValAsnLeuAlaArgAla 548

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Db 2480 GCGGAGAGGCGGTGAACCTGTCTGCGGCGCAGAAAGACGCGGTGAGCTCGCGCGCC 2539  
 QY 549 ValTyrGlnAspAlaAspIleTyrLeuLeuAspAspProLeuSerAlaValAspAlaGln 568  
 Db 2540 GTGTCTCCACGCGGTGACATTTACCTTTCGATGATCCCTCTCCAGCATGATGCCAT 2599  
 QY 569 ValSerArgHisLeuPheGluLeuGlyCysHisGln-----IleLeuHisGluValLeu 586  
 Db 2600 GTGGGAAAAACATCTTTGAAAAATGATGATGGCCCCCAGGGAGATCTGAAAGAACAGAGC 2659  
 QY 587 ThrIleLeuValThrHisGlnLeuGlnTyrLeuValAlaAspGlnIleLeuIleLeu 606  
 Db 2660 CGGATCTTGATCCAGCAGCATGAGCTCTGCGCAGGTGAGCATCATCTGCTCATG 2719  
 QY 607 LysAspGlyLysMetValGlnLysGlyTyrTyrGlnPheLeuLysSerGlyIleAsp 626  
 Db 2720 AGTGGCGGCAATCTTGATGATGAGCTCTACAGAGCTGCTGCTGAGACGCGCGC 2779  
 QY 627 PheGlySerLeuLeuLys-----LysAspAspGlnGlnSer 638  
 Db 2780 TTCCGTGATCTCTGCTGATCTTATGCGACAGACAGAGCAGAGATGACAGAGAAC 2839  
 QY 639 GlnGlnProProValProGly-----ThrProThrLeuArgAsn----- 651  
 Db 2840 GGGGTACAGGCGGTGACGCGTCCAGGAGAGAGAACAGAACAGATGAGCATGCTG 2899  
 QY 652 -----ArgThrPheSerGlnSerSerValTyrSer 661  
 Db 2900 GTGACGAGCAGTGCAGGAGAACATGACAGCATGACAGCTGACGCTCTCCCTCATGAT 2959  
 QY 662 GlnGlnSerSerArgProSerLeuLysAspGlyAlaLeuGlnSerGlnAspThrGln 681  
 Db 2960 GGGGACATCAGAGGACCAACAGACAGCCGACAGAACTGACAGAACTGAGGCCAGAG 3019  
 QY 682 ValProVal-----ThrLeuSerGlnGlnLysAspArgSerGln-----GlyLysValGlyPheGln 699  
 Db 3020 GAGGAGACCTGAGATGATGAGGCTGACAGGCGGACAGAGGAGGATCAAGCTTCC 3079  
 QY 700 AlaTyrLysAsnTyrPheArgAlaGlyAlaHisTyrIleValPhe-----IlePheLeu 717  
 Db 3080 GTGTACTGGACTACATGAGGACCATCGGACTCTTCATCTCTCTCAGCATCTTCTCT 3139  
 QY 718 IleLeuLeuAsnThrAlaAlaGlnAlaTyrValLeuGlnAspTyrPheLysSerTyr 737  
 Db 3140 TTCAATGTGTAC-----CATGTCTCGCGCTGCTTCCAACTATGCTTCAAGCTTC 3190  
 QY 738 TrpAlaAsnLysGlnSerMetLeuAsnValThrValAsnGlyGlyLysValThrVal 757  
 Db 3191 TGGACTGAT-----GACCCCATCGTCAAGGAGCATCAGAGACAGACAGAA 3235  
 QY 758 ---LysLeuAspLeuAsnTyrTyrLeuGlyIleTyrSerGlyLeuThrValAlaThrVal 776  
 Db 3236 GTCCGCGTGAAGCTGATGAGGACCTGAGCATTTTCACAGGATGCGCGCTG----- 3286  
 QY 777 LeuPheGlyIleAlaArgSerLeuValPheTyrValLeuValAsnSerGlnThr 796  
 Db 3287 ---TTTGGCTACTCATGGCCGTGTCACCGGGGAGATCTTG-----GCTTCCCGCTGT 3337  
 QY 797 LeuHisAsnLysMetPheGlnSerIleLeuLysValAlaProValLeuPheAspArgAsn 816  
 Db 3338 CTGCACGTGAGACCTGCTGACAGCATCTGCGGCTACCCATAGACCTTTTAGCGGAC 3397  
 QY 817 ProIleGlyArgIleLeuAsnArgPheSerLysAspIleGlyHisLeuAspLeuLeu 836  
 Db 3398 CCCAGTGGGAACTGATGAAACCGCTTCTCCAGAGAGTGAACAGTGAATCCATGATC 3457  
 QY 837 ProLeuThrPheLeuAspPheIleGlnThrLeuGlnValValGlyValValSerVal 856  
 Db 3458 CCGGAGGTATCAGATGTTTATGAGGCTCTGTTTCACGATCATGATGCTGATCGT 3517  
 QY 857 AlaValAlaValIleProTyrIleAlaIleProLeuValProLeuGlyIleIlePheIle 876  
 Db 3518 ATCTGCTGCGCAGCGCATCGCGCATCATCATCCGCGCTTGAGCTCTTACTTCC 3577

QY 877 PheLeuArgTyrPheLeuGlnThrSerArgAspValLysArgLeuLysSerThrThr 896  
 Db 3578 TTCTCCAGAGCTTCTAGTGGCTTCTCCCGGACAGTGAAGCCCTGATCGGTGAC 3637  
 QY 897 ArgSerProValPheSerHisLeuSerSerLeuGlnGlyLeuTyrThrIleArgAla 916  
 Db 3638 CGCTCCCGGCTATTTCCATTTCAAGAGACTTGTGCGGGGAGAGCGTCAATTCAGACC 3697  
 QY 917 TyrLysAlaGlnGlyArgCysGlnGlnLeuPheAspAlaHisGlnAspLeuHisSerGlu 936  
 Db 3698 TTCCAGAGCAGAGGCGCTTATCCACAGATGACCTGAAGTGAAGAGACAGACAGAG 3757  
 QY 937 AlaThrPheLeuPheLeuThrThrSerArgThrPheAlaValArgLeuAspAlaIleCys 956  
 Db 3758 GCTTATTTCCCGACATGCTGGCCCAACAGTGGCTGGCCGCTGGATGTGTGGGC 3817  
 QY 957 AlamecPheValIleIleValAlaPheGlySerLeuIleLeuAlaLysThrLeuAspAla 976  
 Db 3818 AACTGCATCGTTGTTGCTGCGCTGCTGCGGATCTCCAGGACAGGCTCATGCT 3877  
 QY 977 GlnGlnValGlyLeuAlaLeuSerTyrAlaLeuThrLeuMetCysMetPheGlnTyrCys 996  
 Db 3878 GGGTGGTGGGCTCTCAGTGTCTTACTCATTTGACAGGTACACAGTACTGAACTGGCTG 3937  
 QY 997 ValArgGlnSerAlaGlnValGlnLysMetMetIleSerValGlyArgValIleGluTyr 1016  
 Db 3938 GTTCGATGATCATGAAATGAAACCAACATCGTGGCGTGAAGAGGCTCAAGAGAT 3997  
 QY 1017 ThrAspLeuGlnLysGlnAlaProTyrGlnTyrGlnLys---ArgProProProAlaTyr 1035  
 Db 3998 TCAAGAGTGAAGAGAGAGCCCTGGGAATTCAGAGAGACAGCTCGGCCAGAGCTGG 4057  
 QY 1036 ProHisGlnGlyValIleIlePhePheAsnValAsnPheMetTyrSerProGlyGlyPro 1055  
 Db 4058 CCCGAGTGGGCGCAGTGAATTCGGAACTCACTGCTCGCTCCGACGAGAGACCTTGAC 4117  
 QY 1056 LeuValLeuLysHisLeuThrAlaLeuIleLysSerGlnGlnLysValGlyIleValGly 1075  
 Db 4118 TTCTGTTTCAGGACATCAATGATGATCAAGTCAATGAGGAGAAAGTGGGATCTGAGG 4177  
 QY 1076 ArgThrGlyAlaGlyLysSerSerLeuIleSerAlaLeuPheArgLeuSerGlu---Pro 1094  
 Db 4178 CCGAGGAGAGCTGGGAATCTCTCCCTGACCTGGGCTTATTTCCGATGACAGAGCTGACC 4237  
 QY 1095 GlnGlyLysIleTyrPheAspLysIleLeuThrThrGlnIleGlyLeuHisAspLeuArg 1114  
 Db 4238 GAAAGAGATCATCATGATGATGATCAATCGCAAGATCGGCTGACAGACTCGCC 4297  
 QY 1115 LysLysMetSerIleIleProGlnGlnProValLeuPheThrGlyThrMetArgLysAsn 1134  
 Db 4298 TTCAAGATCACCATCATCTCCACAGACCTGTGTTGTTGTTGGGTGCTCCCTCGAATGAC 4357  
 QY 1135 LeuAspProPheAsnGlnHisThrAspGlnGlnLeuTyrPheAlaLeuGlnGlnValGln 1154  
 Db 4358 CTGACCCATTCAGCAGTACTCGGATGAAAGCTGAGAGCTCCCTGAGCTGCGCCAC 4417  
 QY 4418 CTGAAGAGCTCGGTGACCGCTTCTCTGCAAGGTGAACCATGATGAGAGAGCGCGG 4477  
 QY 1175 SerAsnPheSerValGlyGlnArgGlnLeuValCysLeuAlaArgAlaIleLeuArgLys 1194  
 Db 4478 GAGAACCTCAGTGTGCGGACGCGCAAGCTTGTGTGCTTGAAGCCCGGCTCTGAGAG 4537  
 QY 1195 AsnGlnIleLeuIleIleAspGlnAlaThrAlaAsnValAspProArgThrAspGluLeu 1214  
 Db 4538 ACGAAGATCTTGTGTGATGAGGACAGGCAAGCTGAGCTGGAACAGAGCACTC 4597  
 QY 1215 IleGlnLysLysIleArgGlnLysPheAlaHisCysThrValLeuThrIleAlaHisArg 1234  
 Db 4598 ATCCAGTCCACATCCGAGACAGTGAAGATGAGACGCTGCTTCACATGACGCCACCGG 4657



Qy	410	ValHisValGlnAspPheThrAlaPheThrAspIysAlaSerGluThrProThrIleuGln	425
Db	1930	ATCATCTGGAAGAAATGCAACCTTCACTTGGGCGAAG---GGTGAACCTCCACACTGGAT	1986
Qy	430	GlyLeuSerPheThrValArgProGlyGluLeuAlaValGlyProValGlyAla	449
Db	1987	GGCATTACACCTTCTCCATTCCTGAGAGAACCTTTGTGGCCGTGTGGGCAAGTAGGCTGC	2048
Qy	450	GlyIysSerSerLeuLeuLeuSerAlaValIleuGlyGluLeuAlaProSerHisGlyLeuVal	469
Db	2047	GGAAAGTCATCTCTGCTGTCAGCCCTGCTGGCTGATGATGACAAGGTGAGAGACATGTG	2106
Qy	470	SerValHisGlyAlaGlyIleAlaTyrValSerGlnGlnProThrPvalPheSerGlyThrIleu	489
Db	2107	ACTCTCAAGGGGCTCCGTGGCCCTACCTGGCCCAAGCGAGGCTGGATTCAAGATGACTCTTC	2166
Qy	490	ArgSerAsnIleLeuPheGlyLysLysTyrGlyLysGlyArgTyrGlyLysValIleLys	509
Db	2167	CGAGAGAACATATCTTTTGGGCAACCCCTGCAGGAAATTACTACAGGCAAGTATGGAA	2228
Qy	510	AlaCysAlaLeuLysLysAspLeuGlnIleuLeuGlnAspGlyAspLeuThrValIleGly	529
Db	2227	GCGTGTGCTCTTCTCCAGATTGTGGAATTCGGCCCACTGGGAGACGGACAGAGATCGGT	2286
Qy	530	AspArgGlyThrThrLeuSerGlyGlyGlyLysAlaArgValAsnLeuAlaArgAlaVal	549
Db	2287	GAGAAAGGTGTGAACCTGTCAAGGGGGCCAGAAAGCAGCTGTGAGCTGGCCGGGCTGTG	2348
Qy	550	TyrGlnAspAlaAspIleTyrIleuLeuAspAspProLeuSerAlaValAspAlaGlyVal	569
Db	2347	TACTCTAATCTGCATATCACTTACTCTTTATATGACCCCTCGGCTGGCTGATGACATGTT	2406
Qy	570	SerArgHisLeuPheGlyLeuCysIle-----CysGlnIleLeuHisGlyLysIleThr	587
Db	2407	GGGAAGCACATCTTTGAGAAGGTGTGTGCTCCATGGGCTTACTAAGAACAGACACGG	2466
Qy	588	IleLeuValThrHisGlnLeuGlnTyrIleuLysAlaAlaSerGlnIleLeuIleLys	607
Db	2467	ATCTGCTGACCCCATGATGATCAGTACTGCCCCCAAGTGATGATCATTTGTCATGAGT	2526
Qy	608	AspGlyLysMetValGlnIysGlyThrTyrThrGluPheLeuLysSerGlyIleAspPhe	627
Db	2527	GGCGGCAAGATCTCAGAGATGGGTCTTATCAGAGCTGTACAGCCGGAGTGGGCTTTC	2586
Qy	628	GlySerLeuLeuLys-----LysAspAsnGln	636
Db	2587	GCTGAGTTCCTGGCGACCTATGCCAACGCTGAGCAGACCTGGCTCGAGAGATGACAGT	2648
Qy	637	GluSer-----GluGlnProProValProGly-----ThrProThr	648
Db	2647	GTCAGTGGTTCAGGGAGAGAGTCAAAAGCGGTGAATAATGGAGTCTGTGTACAGACACC	2706
Qy	649	Leu-----ArgAsnArgThrPheSerGluSerSerValTyrSerGlnGlnSerSer	665
Db	2707	GTAGGAAAGCACTGCAAGAGGATCTCAGCAACTGTCTTCCACAGTGGGGATATACAGC	2766
Qy	666	ArgProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGlnAsnValProValThr	685
Db	2767	CAGCAACACAGCAGATACCGCAATCTTGAGAGAGCTGAGACTGAGAGAGACAGCTGAGAG	2826
Qy	686	LeuSerGlnGluAsnArgSerGlu-----GlyLysValGlyPheGlnAlaTyrIleAsnTyr	704
Db	2827	CTAATGAGAGCAGAGAAAGGCCAGACAGGGCAGGTGCAGCTGCATGTATCTGACATAC	2886
Qy	705	PheArgAlaGlyAlaHisTyrIleValPhe-----IlePheLeuIleLeuLeuAsnThr	722
Db	2887	ATGAAGGCCATTGGGCTGCTCATCACTCTTGAAGTATCTTCTTCTGTCACAC---2943	2943
Qy	723	AlaAlaGlnValAlaTyrValLeuGlnAspTyrThrPheLysTyrTyrAlaAsnLysGln	742
Db	2944	-----CATGTATCTGCAGCTGGCTCTTAACTATTTGGCTGAGCTCTTGCAGACATCCC	2997

OY	743	terheteuleuhsenalThrrValaAnglyGlyValysanValThrglyLysleuAspLeuhsn	762
Db	2998	CTGTGTTCATGGGACT-----CAGGGCAACAGAAAT	3030
OY	763	TrpThryleuGlyIleTySer-----GlyLeuthrValAlathrValleuPheGlyTle	780
Db	3091	TTTGCGGTGAGTGTCTATGGGGCTTGAGGACCTTGCMAAGGTGACGAATATTGGCTAC	3090
OY	781	AlaArgSerLeuLeuValPheTyValleuValAsnSerSerGlnThrLeuHisAsnLys	800
Db	3091	TCCATGGCTGTGTCCATCGGGGACATCTTT-----GCTCCCGCTGTTCACCTGGAC	3144
OY	801	MetPheGluSerIleLeuLysAlaProValleuPhePheAspArgAsnProIleGlyArg	820
Db	3145	CTGCTATACAAATGTTCTTCATCCACCAATGAGTGTTCAGAGCTACACCAAGTGGGAC	3204
OY	821	IleLeuAsnArgPheSerLysAspIleGlyHisleuAspAspLeuLeuProLeuthrPhe	840
Db	3205	CTATGGAACCAATCTCTCCAGAGACTGGACACAGTGAATCCAGATCCCGCAGTCACTC	3264
OY	841	LeuAspPheIleGlnThrLeuGlnValValGlyValValSerValAlaValAlaVal	860
Db	3265	AAGATGTTCAATGGGTCACTTCCTCAGTGTCAATGAGCTGTCAATCATCTCTAGCC	3324
OY	861	IleProThrPheAlaIleProLeuValProLeuGlyIleIlePheIlePheLeuAspArg	880
Db	3325	ACGGCCATTCGCCGAGTCATCTCCACCTTCGGGTGTGTTCCTTGTGTGCAGAGG	3384
OY	881	TyrPheLeuGlnThrSerArgAspValLysArgLeuGluSerThrThrArgSerProVal	900
Db	3385	TTCTATGGCTTCTCTCAAGCACTGAAGGCTGTGAGTGTGCAGCCGTTCCCTGTG	3444
OY	901	PheSerHisLeuSerSerSerLeuGlnGlyLeuThrThrIleArgAlaTyTyLysAlaGlu	920
Db	3445	TACTCACACTTCATGAGACCTTGTGGAGTCACTGTCATCGTGTTCCTTTGAGAGACAG	3504
OY	921	GluArgCysGlnGluLeuPheAspAlaHisGlnAspLeuHisSerGluAlaThrPheLeu	940
Db	3505	GAGGCTTCATTCACCAAGATGACCTGAAGTAAATGAAGCAACGAAGGCTTCACTCC	3564
OY	941	PheLeuThrThrSerArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheVal	960
Db	3565	AGCATGTGGCCAAACAAATGGCTTGTGTGCGCTTGAAGTGTGGGCACTGCATTTGTG	3624
OY	961	IleIleValAlaPheGlySerLeuIleuAlaLysThrLeuAspAlaGlyGlnValGly	980
Db	3625	CTGTTCGTGCTCTTGTTCAGATCATCTCCGGCAGACGCTCAATGCTGGTGTGGGC	3684
OY	981	LeuAlaLeuSerTyralaLeuThrLeuMetCylMetPheGlnTrpCysValArgGlnSer	1000
Db	3685	CTCTCTGTGTCTTACTCACTGCAGATATACATCACTTGAACCTGGCTGTTCGATGTCC	3744
OY	1001	AlaGluValGluAsnMetMetIleSerValGluArgValIleGlyTrpThrAspLeuGlu	1020
Db	3745	TCGAGATGAGAGACCAACATTTGGCAGTGGAGAGACTGGAAGAGTATTCGAACACAG	3804
OY	1021	LysGlnAlaProTrpGluTyrglnLysArgProProProAla---TrpProHisGluGly	1039
Db	3805	AAGAGGCTCTTGGCAATTCGAGAAACAGCTCACCCGACACTGGCCCATTCAGGC	3864
OY	1040	ValIleIlePheAspAsnValAsnPheMetTySerProGlyGlyProLeuValLeuLys	1059
Db	3865	CGTGTAGGTTCGGAGATTACTGCTGAGGATACGAAGAAGCTTGAGCTTGATTCAG	3924
OY	1060	HisleuThrAlaLeuIleLysSerGlnGluLysValIleValIleValTyArgThrGlyVal	1079
Db	3925	CACATTAATGTCAACATTGAGGGTGAAGAAAGGTGGTATGTGAAGTCTGAACGGAGCT	3984
OY	1080	GlyLysSerSerLeuIleSerAlaLeuPheArgLeuSerGlu---ProGlnGlyLysIle	1098
Db	3985	GGGAATCATCTCTCACCTGGGTTTGTTCGGATCATAGATGTGCAAGAGGGGAATC	4044
OY	1099	TrpIleAspLysIleLeuThrThrGlnIleGlyLeuHisAspLeuArgLysMetSer	1118



QY 335 ThrPheThrThrValLeuLeuGly-----SerValIleThrAlaSerArgValPhe 352  
 DB 1693 ACCTTGGCTGCTTTGTGACTGTGACGAGAAAGAACATCTTGAAGCAAGAAAGACCTTT 1752  
 QY 353 ValAlaValThrLeuTyrGlyAlaValArgLeuThrValThrLeuPhePheProSerAla 372  
 DB 1753 GATATCCCTGACCTGTTCAATATCTTGCCGCTTCCCACTCAACATC---CTACCCCATGTC 1809  
 QY 373 IleGluArgValSerGluAlaIleValSerIleArgArgIleGlnThrPheLeuLeu 392  
 DB 1810 ATCAGACGATGTGTCAGGCGGAGGCTGCTCAAGCGTCTCAGATCTTGTGCTCAC 1869  
 QY 393 AspGluIleSer-----GlnArgAsnArgGlnLeuProSerAspGlyLeuLys 408  
 DB 1870 GAGGAGCTGAGACCCAGACGATCGAGCATGTGATCAAGATGCTGAGAGGATGAT 1929  
 QY 409 MetValIleValGlnAspPheThrAlaPheTyrAspLysAlaSerGluThrProThrLeu 428  
 DB 1930 AGCATCACTGAGAAATGCAACTTCACTGGGCCAGG---GATGAACTCCCACTG 1986  
 QY 429 GlnGlyLeuSerPheThrValArgProGlyGluLeuLeuAlaValGlyProValGly 448  
 DB 1987 AATGCAATCACTTGCCGCACTGATGAGGCTTGTGCGGTGGCGGAGGATGAGC 2046  
 QY 449 AlaGlyLysSerSerLeuLeuSerAlaValLeuGlyGluLeuAlaProSerHisGlyLeu 468  
 DB 2047 TGTGGAAATCACTCTGCTGTGACGCTGCTGCTGAGATGACAAAGTGAAGGACAT 2106  
 QY 469 ValSerValIleGlyAlaArgIleAlaTyrAlaSerGlnGlnProTyrValPheSerGlyThr 488  
 DB 2107 GTGACTCTCAAGGGCTCCGCTGCTATGTCGCCAGAGGCTGATTCAGAAATGACTCT 2166  
 QY 489 LeuArgSerAsnIleLeuPheGlyLysLysTyrGlyLysGluArgTyrGlyLysValIle 508  
 DB 2167 CTCCAGAGAAATCACTGTTTGGGCGCCCTCAGAGAAATGCTTCAAGCGGTGATG 2226  
 QY 509 LysValaCysAlaLeuLysLysAspLeuGlnLeuGluAspGlyAspLeuThrValIle 528  
 DB 2227 GAGGCTGTGCTCTCTCCGATTTGGAAATCTTCCAGTGGGAGCTTCACAGAGATT 2286  
 QY 529 GlyAspArgGlyThrThrLeuSerGlyGlyGlnLysValaArgValAsnLeuAlaArgAla 548  
 DB 2287 GGTGAAGAGGTGTGAACCTGTCCGGGGGCGCAGAAAGACGCTGAGCTGCTGGGGT 2346  
 QY 549 ValTyrGlnAspAlaAspIleTyrLeuLeuAspAspProLeuSerAlaValAspAlaGlu 568  
 DB 2347 GTGTATTGTAACTGTGACATCTTAACTTGAAGCAGACCCCTCTCGAGCTGTGATGACAT 2406  
 QY 569 ValSerArgHisLeuPheGluLeuCysIle-----CysGlnIleLeuHisGluLysIle 586  
 DB 2407 GTTGGAGACACATCTTGAAGAGGTGTGGGCTCCATGGGCTTACTGAAGAACAGACA 2466  
 QY 587 ThrIleLeuValThrHisGlnLeuGlnIleTyrLeuLysValaAlaSerGlnIleLeuLeu 606  
 DB 2467 CGGATCCGTGTGACCCATGATGATCACTGACCTGCCCCAAGTGAATGATCATTTGTCAATG 2526  
 QY 607 LysAspGlyLysMetValGlnLysGlyThrTyrThrGluPheLeuLysSerGlyIleAsp 626  
 DB 2527 AGTGGCGGAGATCTCAGAGATGGATCTTATCAGAGAGCTCTGACCGGATGGGCGC 2586  
 QY 627 PheGly-----SerLeuLeuLysLysAspAsn 635  
 DB 2587 TTTGCTGAGTTGTGGCGACCTATGCAACACTGAGAGAGCTGCTTCAAGAGATGAC 2646  
 QY 636 GluGlnSer-----GluGlnProProValPro----- 644  
 DB 2647 AGTAAGAAATGTGTGAGTGTTTAAGGAAGAGTCAAAAGCGGTGAAAAATGGATATCTG 2706  
 QY 645 -----GlyThrProThrLeuArg-----AsnArgThrPheSerGlyLys 657  
 DB 2707 GTGACAGACGAGTGAAGGCGCTGACAGAGCATCTCAGCAACTCTTCTTCCACAGT 2766  
 QY 658 SerValTyrSerGlnGln-----SerSerArgProSerLeuLysAspGlyValaLeuGlnSer 676

DB 2767 GTGCTTACTAACCGACACAGACAGACAGCCGAGCTGCAAGAGTCTGGGTTAAAGAG 2826  
 QY 677 GlnAspThrGluAsnValProValThrLeuSerGlyGluAsnArgSerGlu-----GlyLys 695  
 DB 2827 GAGACTTGGAG-----CTGATGGAAGCAGACAGGCGCCAGACAGGCGAG 2871  
 QY 696 ValGlyPheGlnAlaTyrLysAsnTyrPheArgAlaGlyAlaIleStrIleValPhe--- 714  
 DB 2872 GTGAAGCTTCCGCTGATGAGACTACATGAAGCCATTTGGCTCTGATCTCTCTTGG 2931  
 QY 715 ---IlePheLeuIleLeuLeuAsnThrAlaIleGlnValaIaTyrValLeuGlnAspTyr 733  
 DB 2932 AGTATCTTCTTTCCTGTGCAT-----CATGATGTGACCTGCTTCAATCAT 2982  
 QY 734 TyrLeuSerTyrTyrAlaAsnLysGlnSerMetLeuAsnValThrValaAsnGlyGly 753  
 DB 2983 TGGTGAATCTCTGACAGATGAGACCGCTCTGTCATGAGACTCAGAG----- 3033  
 QY 754 AsnValThrGluLysLeuAspLeuAsnTyrTyrLeuGlyIleTyrSerGlyLeuThrVal 773  
 DB 3034 AACAGAAATTTTCACTAAGTCTATGAGGCTTGGGCACTTGCAGAGTGTGCACTA 3093  
 QY 774 AlaThrValLeuPheGlyIleAlaArgSerLeuLeuValPheTyrValLeuValaAsnSer 793  
 DB 3094 -----TTGGCTATTCCATGCTGTGTCCATTTGGGGGATCTTT-----GCC 3135  
 QY 794 SerGlnThrLeuHisAsnLysMetPheGluSerIleLeuLysValaProValLeuPhePhe 813  
 DB 3136 TCCCGTCCCTGACACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3195  
 QY 814 AspArgAsnProIleGlyAlaArgIleLeuAsnArgPheSerLysAspIleGlyHisLeuAsp 833  
 DB 3196 GAGGTACACCAAGTGGAGACCTAGTGAACGATTTCTCAAGAGTGTGACACAGTGGAC 3255  
 QY 834 AspLeuLeuProLeuThrPheLeuAspPheIleGlnThrLeuLeuGlnValaGlyVal 853  
 DB 3256 TCCATGATCCCGCAGAGTATGAAGTTCATGAGTTCATGAGTTCATGAGTTCATGAGTTC 3315  
 QY 854 ValSerValaValaValaValaIleProTyrIleAlaIleProLeuValaProLeuGlyIle 873  
 DB 3316 GTCAT 3375  
 QY 874 IlePheIlePheLeuAspArgTyrThrLeuGlnThrSerArgAspValaLysArgLeu 893  
 DB 3376 GTTAACTTGTGTGCAAGGATTTATGTGCTCTCTTCAAGTGAAGTGAAGGCTGAG 3435  
 QY 894 SerThrArgSerProValPheSerHisLeuSerSerLeuGlnGlyLeuTyrThr 913  
 DB 3436 TCTGCACTGCTTCCCTGTGTACTACACTTCAATGAGACTTCTGAGGAGTCACTGTC 3495  
 QY 914 IleArgAlaTyrLysAlaGluGluArgCysGlnGluLeuPheAspAlaHisGlnAspLeu 933  
 DB 3496 ATCCGTGCTTGAAGAACAGAGGCTTCAATGCGCAAAAGTCACTGAAGTGAAGTGAAG 3555  
 QY 934 HisSerGluAlaTyrPheLeuPheLeuThrThrSerArgTyrPheAlaValaArgLeuAsp 953  
 DB 3556 AACCAAGAGGCTTACATCCAGATTTGTGCAACAGAGTGTGCTGTGCGCTGAG 3615  
 QY 954 AlaIleCysAlaMetPheValIleIleValaIlePheGlySerLeuIleLeuAlaLysThr 973  
 DB 3616 TGTGTGGCACTGATGCTGTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3675  
 QY 974 LeuAspAlaGlyGlnValaGlyLeuAlaLeuSerTyrAlaLeuThrLeuMetGlyMetPhe 993  
 DB 3676 CTCACTGCTGCTGT 3735  
 QY 994 GlnTyrCysValaArgGlnSerAlaGluValaGluAsnMetIleSerValaGluArgVal 1013  
 DB 3736 AACTGTGATGTCGAATGCTCTGAGATGAGAACCAATGAGGAGTGAAGAGTGAAGTGAAG 3795  
 QY 1014 IleGluTyrThrAspLeuGluLysGluAlaProTyrGlyLysArgProProPro 1033

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Db      3796 AAGAAATATTCGAAACGAGAGAGGCTTCTGGCAATCCAGACAGCTCCACC 3855
      1034 Ala---TTPProHiegluYValIleIlePheAspAsnValAsnPhMetYrSerPro 1052
      3856 AGCACCCTGGCCCATTCAGGCGCGGTAGAGCTTCGGGATTAATCTGCTTGAAGTACAGAA 3915
      1053 GtYgYProLeuValIleuYshiIseuThraIaleuIleYseIingluYValIglY 1072
      3916 GACTTGACCTGGTCTTCAAGCACAATAATGTCAACATGAGGCTGAGAAAGGTTGGT 3975
      1073 ILevalIglYrThrglYValIleIleYserSerIleuIleSerIaleuPheArgLeuSer 1092
      3976 ATTGGGTGCTGACAGAGCTGGAAATATCTCTCAACCTGGGTTGTTCCGATCAAT 4035
      1093 Glu---ProgluYglYserIleTrpIleAspYsIleLeuThrThrglIleglYleuHis 1111
      4036 GAGTCGACAGAGGAGAGATCATCATGATGGATTAACATGCTTAAGTTGGCCGCGAC 4095
      1112 AspLeuArgYLeuYMetSerIleIleProgluYProValIleuPheThrglYThrMet 1131
      4096 AACCTGCGCTTCAAGATCACCATTCATCCACAGATCTGTTTGTCCCGGCTTCCCTC 4155
      1132 ArgYLeuAspLeuAspProPheAsnGluIleThraAspGluYLeuThraAsnIaleuGlu 1151
      4156 CGCATGACCTGGACCTTTCAGTCAAGTATCTGATGAAGAAAGTGTGAGTGTGGAG 4215
      1152 GluValIgluYleuYsIleuThrglIleIleAspLeuProglYleuMetAspThrglIleuAla 1171
      4216 CTTCCTCACCTGAAGGGCTTTGTGTGAGCTTGCCTGACAGCTGACATGAGTGTGA 4275
      1172 GluSerGlySerAsnPheserValIglYIleArgIleuValIcyLeuAlaArgIale 1191
      4276 GAAGGTGAGAGATCTGAGTGTGGGCGACGACAGCTGTGTGCTGGCCGCGCTTGG 4335
      1192 LeuArgYLeuAsnGluIleuIleIleAspGluIleThraAsnValAspProArgThr 1211
      4336 CTGAGGAAACAAAGATCTAGGTGAGAGGCTGACAGCTGTGATCTGGAGAA 4395
      1212 AspGluLeuIlegluYleuYsIleArgYleuYsPheAlaIleCyThrValIleuThrlle 1231
      4396 GATGACCTTATTCAGTCCACCGTCCGAGAGCATTTGAAGACAGTATGCTGCTCACTAT 4455
      1232 AlaHieArgYLeuAsnThrlIleIleAspSerAspYsIleMetValIleuAspSerGlyArg 1251
      4456 GCTCATCGGCTGAATCATTAATGACTATACAGGGGATGTGCTCGAACAAGAGAA 4515
      1252 LeuYsGluYrAspGluProYrValIleuLeuGluAsnYleuGluSerIleuPheYrYls 1271
      4516 ATTGGGAGGTGTGTGACCCCTCTGAGCTCTGCAAGAAAGAA--GGCGTCTTCTATAGC 4572
      1272 MetValIgluYleuYglY 1277
      4573 ATGGCCCAAGATGTGCG 4590

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RESULT 12  
US-10-932-182A-484

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; Sequence 484, Application US/10932182A
; Publication No. US2006004625A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHITIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIRO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 484
; LENGTH: 4551
; TYPE: DNA

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; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-484
Alignment Scores:
Pred. No.: 1,096-203
Score: 2227.00
Percent Similarity: 56.64
Best Local Similarity: 37.44
Query Match: 32.84
DB: 7
Gaps: 23
US-09-976-858-42 (1-1325) x US-10-932-182A-484 (1-4551)
      4 ValYrGluYValIle-----LysProAsnProLeuGluIleAspAlaAsnLeuCySer 20
      598 ATACATCAGAAAGTGTATGAGAAAGAAACCAAGCCGTCAGATAGCTTAATATATTCCTCC 657
      21 ArgValIlePheIleTrpIleuAsnProLeuPheYsIleGluYleuYsArgYleuGlu 40
      658 AGAATTCATATTTCTTGATGTCAAGTTTAATGAAGAACTGGATATGAAGAAATACCTGATA 717
      41 GluAspAspMetYrSerValIleuProGluAspArgSerGluIleIleGluYgluYleu 60
      718 GAGCTGATTTGTATTAATTAACAAAAAATTAGTACAGACAGAACTCTCAGAAATTA 777
      61 GlnGluYrPheTrpAspYsGluValIleuArgIleGluAsnAspAlaGluYsProSerIleu 80
      778 GAGAAATATGGCAAAATGAAGAACTT-----AAGCATTAATCAAAACCTTCCTTA 825
      81 ThrArgAlaIleIleYleuCySerYrTrpYsSerYrIleuValIleuGluYIlePheThrlleu 100
      826 TCTGGGCTATATGCAAAACCTTTGGATATTAATATGTTTAAAGCCGCTTCTCAAGACC 885
      101 IlegluYserAlaYleuValIleIleProIlePheLeuGluYsIleIleAsnYrPhe 120
      886 ATTCAATGATTTCTGCGATTTGCTGCAACACACATTAACAAATTTTAATCAAGTTGTT 945
      121 GluAsnYr-----AspPromet-----Asp 127
      946 ACCGACTCAATTAAGAAAGCAAGATGATGACATCTTAACCTGCGATATGATGAT 1005
      128 SerValIleuAsnThrlAlaYrAlaYrAlaThrlValIleuThrlPheCyThrIleu 147
      1006 AAGCTGTATCAAAATTCGCCATTAATGAAGGTTTAAATGATGCGTTTTCATATGTTCT 1065
      148 LeuAlaIleuHis-----HisLeuYrPheYrYrHisValIleGluYleuGluY 163
      1066 GTGGGTTTACTCAAAACATCTGTGCTGATCAATATTTTGAATGCTTTTAACCTGCT 1125
      164 MetArgLeuArgValIleMetCyshiIleYrYrArgYsAlaIleuArgLeuSerAsn 183
      1126 ATGTATGTCAAAAGGCTTGTGATGCTGCTGATATCAAAAGGCTTTAGTTTATCTAAT 1185
      184 MetAlaMetGlyYsThrlThrglYgluYIleValIleuLeuLeuSerAsnAspValasn 203
      1186 GAAGATCTGACCTTCATCTTACTGTGACATCTGTAATTTTAATGAAGGTGAGTGCAGAA 1245
      204 LysPheAspGluValIleThrlPheLeuHisPheLeuThrlAlaGluYProLeuGluAlaIle 223
      1246 AATTCACAAAGATCTACATCAATGTTAATTTGATTTGTCAGGCGCTTTCAGATTAAT 1305
      224 AlaValThrlAlaLeuLeuTrpMetGluIleGluYleuSerCyValIleGluYMetAlaVal 243
      1306 ATCTGTCTTACTCTTTGATTAAGATTAATGGGTAATTCAGATGTGGGTGATATCATATA 1365
      244 LeuIleIleLeuLeuProLeuGluIleSerCyPheGluYsLeuPheSerSerLeuArgSer 263
      1366 CTAGTTGTATGATGCCATTAATTAATTCATTTTAATGAAGAAATCAAAAGAAATTAACAAA 1425
      264 LysThrlAlaThrlPheThrlAspAlaArgIleArgThrMetAsnGluValIleThrlGlyle 283
      1426 TCTCAATGAATATCAAGAGCAAGAAAGAACTGTGTATTAATGAAATTTCTAAACAACATC 1485

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QY	284	ArgIlelleIyMerTyrAlaTrgIuIySerPheSerAenulleIleThraSneIuehrg	303
Db	1486	AAATCTCGAAATTTATATGCGGGGAAAAGCCTTACAGGAGAAAGTTCGAAACGTTGA	1545
QY	304	--LysIySGuIIleSerIyIleIeuhrgSerSerCySleuArgIyMeCaSneIueIa	322
Db	1546	AATACCAAGAACTAAATATTAATTAACATAATTGGTCTATATGCGCTGTAACAATTTC	1605
QY	333	SerPhePheSerAlaSerIySleIleValPheValThrPheThrThrValIeIueu	342
Db	1606	CAATTTAACATAGTTCCTTTCTTCTAGTTTCATGCTGACGTTGCTGCTTGTGACACC	1665
QY	343	---GlySerValIleThraIleSerArgValPheValAlaValThreUtyrGlyAlaVal	361
Db	1666	GAAGATAGGCGCTTACTACCGATCTAAATTTTCCTGGTTTAACTTTTCAATCTACTT	1725
QY	362	ArgIeuthrValThreUhePhePheProSerAlaIleGluArgValSerGluAlleVal	381
Db	1726	TCATTTCCATTC--ATGATTAATTCCTCAAGTTTGAATTCATTAATCGAAGCTTCTGT	1782
QY	382	SerIleArgArgIleGlnThrPheIeuleuIeuhgIuIleSer-----Gln	397
Db	1783	TCTATTTGATAGGCTATTTCTCTTTTTCACATGAGAGGCTACACCGAGATTCGTGTGAG	1842
QY	398	ArgAenAArgIuIeuhProSerAhpGlyIySlySmetValIleVal--GlnAhpPheThr	416
Db	1843	CGCTTACCAAAAGTGAAGAAATGTTGGTATATAGCCATCAATATTTGGCAGACGCTACC	1902
QY	417	AlaPheTSPApIyAlaSerGlu--ThrProThraGlnGlyIeuhSerPheThrVal	435
Db	1903	TTTTTATGGCAACGTAAACCGAATATATAAGTACGCTTGAATAAATATCAATTTCCAGCT	1962
QY	436	ArgProGlyIuIeuhIeulAlaValGlyProValGlyAlaGlyIySerSerIeuh	455
Db	1963	AAGAAAGGAGATTAACCTGATTTGTTGGTAAAGTTGATGGAGAAACCGCTTATTA	2022
QY	456	SerAlaValIeuhGlyIuIeuhIaProSerHISgIyIeuhValSerValHISgIyArgIle	475
Db	2023	TCAACCAATTTGGGAGCTTATTTAGATCAAAAGGCTTGGCTCAGTCCAGCGTATAGTGT	2082
QY	476	AlaTyrAlaSerGlnGlnProTrpValPheSerGlyThrIeuhArgSerAenIleuPhe	495
Db	2083	GCATACGTCACAAAGTTCATGAGATATGAATGGAGACGTCACAAAGAAACATTTGTTT	2142
QY	496	GlyIySlyTyrGluIySgIuArgIyTyrGluIySValIleIyAlaCyAlaIeuhIyS	515
Db	2143	GGGCAATAGTACGATCGTCACTTTATATGAAAAACTATCAAGGCTGTGCGTTAACATT	2202
QY	516	AhpIeuhGlnIeuhGluAhpGlyAhpIeuhThrValIleGlyAhpArgGlyThrThreU	535
Db	2203	GACTTGGCAATTTTATGATGATGATGATTAAGACGTAAATTTGGTGAAGAAAGGATATTCCTTG	2262
QY	536	SerGlyIyGlnIyAlaArgValAenIeuhIaAgaIaValTyrGlnAhpAlaAhpIle	555
Db	2263	TCGGCGGCGCAAAAGCAAGCTTATCTTACGACAAAGAGATTTATTCAAAGGCGAGATCT	2322
QY	556	TyrIeuhIeuhAhpAhpProIeuhSerAlaValAhpAlaGluValSerArgHISleuPheGlu	575
Db	2323	TATCTACTGACGATCCCTTGGCGGCTGTGACAAACACGTGGCTAGGCAATTTGGTCAA	2382
QY	576	IeuhCyAlaCySgIu-----IleuHISgIuIySleIleuValThrHISgIu	593
Db	2383	CATGATATGGGTTCAAAATGTTTACTTCAATTCCAAAACCAAGTTATTTGGCAACGAAACAA	2442
QY	594	IeuhGlnIyIeuhIyAlaIleSerGlnIleuIleIeuhIyAhpGlyIySmetValGln	613
Db	2443	GTAAAGCGCTTATCTGTGGCAAGTTCATTCATTAATGATTAATGATGAATTAATTTCAA	2502
QY	614	IySgIyThrTyrThrGluPheIeuhIySerGly-----Ile	625
Db	2503	CAGGAGCACTATGATGATATTAACAAGACGCGGACCTCCCTGTTGGAATTAATCAAC	2562
QY	626	AhpPheGlySerIeuhIeuhIyAhpAenGluIySerGlnIyProValIyProGly	645

DB 2553 GATTATGCT-----AAAACACAAATATATACACACGCAACCACTGATCTCA 2613  
 QY 646 ThrProThrLeuArgaAnaArgThrPheSerGluSerSerValTrpSerGlnInSerSer 665  
 DB 2614 ACTAACTCAATTCGCGAAAACAGATATCCGATTGAAGCGCAGCTGGACAAATTAACAAAA 2673  
 QY 666 ArgProSerLeuLysaBpGlyAlaLeuGlnSerGln----- 677  
 DB 2674 CTAAATGATCTGATTTCCGCACCGCTGACCTCAAGCTTAAGAGAGCTAGTATGCA 2733  
 QY 678 -----AspThrGlnAsnValProValThrLeuSerGln 689  
 DB 2734 ACTTTACCGCAGTATGATTTTGGCGATGATGAAAACGTT-----GCTAAAGAGAA 2784  
 QY 690 AsnaArgSerGlnGlyLysValGlyPheGlnAlaTyrLysaAsnTyrPheArgAlaGlyAla 709  
 DB 2785 CATGTGAACAGCGGAAGGTGAAGTGAACATTTACTACAGTACCGTAAAGCTGTGAAC 2844  
 QY 710 HisTrpIleValPheIlePheLeuIleLeuLeuAsnThrAlaGlnValAlaTyrVal 729  
 DB 2845 CCAAAAAGTGTTCGTGGTTCATATGTTATCTTCA-----GTTATATCAATGTTCTCATCCGTC 2901  
 QY 730 LeuGlnAspTrpTrpLeuSerTyrTrpAlaAsnLysGlnSerIleLeuAsnValThrVal 749  
 DB 2902 ATGGGATACGTTTGCGTGAACACTGGTCCGAAGTTATATGCCGCTATGGCGCTAATCCG 2961  
 QY 750 AsnGlyGlyGlnAsnValThrGlnLysLeuAspLeuAsnTrpTyrLeuGlnIleTyrSer 769  
 DB 2962 AATGCTGCTGCT-----TACTGGGTATCATATTC 2991  
 QY 770 GlyLeuThrValAlaIleThrValLeuPheGlyIleAlaArgSerLeuValPhe--Tyr 788  
 DB 2992 GCCCTTGGATTTGGTTCAGCGTTGGCAACTTATATCAGACTATGTTCTTTGGGCTAC 3051  
 QY 789 ValLeuValAsnSerSerGlnThrLeuHisAsnLysMetPheGlnSerIleLeuLysAla 808  
 DB 3052 TGCACTATTCATGCTCCAAATATTTTGACACAACTGTGACAAACTGTGGCTAAGAGCT 3111  
 QY 809 ProValLeuPhePheAspArgaAsnProIleGlyArgIleLeuAsnArgPheSerLysAsp 828  
 DB 3112 CCATGACCTTTTGCAGAACACACCGATGTGGTGAATTTTAAACGTTTTTGCATGAT 3171  
 QY 829 IleGlyHisLeuAspAspLeuLeuProLeuThrPheLeuAspPheIleGlnThrLeuLeu 848  
 DB 3172 ATATATTAAGTGAAGCTTGTTGGTGGAAAGACCTTTTCTCAGTTTTCGATAGCGGTA 3231  
 QY 849 GlnValValGlyValLysSerValAlaValAlaValIleProTrpIleAlaIleProLeu 868  
 DB 3232 AAAGTTTCAGTTTACTATCTACTGTTATTTGTCGACCAACGTCGCAATTCATTTTATATC 3291  
 QY 869 ValProLeuGlnGlyIleIlePheIlePheLeuArgTyrPheLeuGlnTrpSerArgAsp 888  
 DB 3292 GTTCATTTGGGTGGTGTTTTACATTTACTATCAACAGTACTATTTAAGAGATCAAGGAG 3351  
 QY 889 ValLysArgLeuGlnSerThrThrArgSerProValPheSerHisLeuSerSerSerLeu 908  
 DB 3352 TTGGCGGTGATTGAATCTATCAACAAGGCTCCAAATTTATCTCATTTTCAAGAAACTTGG 3411  
 QY 909 GlnGlyLeuTrpThrIleArgAlaTyrLysAlaGlnGlnArgCysGlnGlnLeuPheAsp 928  
 DB 3412 GGCGGTCTTCGTACAGTTAGGTTATTCACACCAAAAGATTTTTCACACATTAATCA 3471  
 QY 929 AlaHisGlnAspLeuHisSerGlnAlaTrpPheLeuPheLeuThrThrSerArgTrpPhe 948  
 DB 3472 TGTGTGATGATATATACAGAGGCGCTTTTATTCCTTCGTCAATCGTATCGTTGGTGG 3531  
 QY 949 AlaValArgLeuAspAlaIleCysAlaMetPheValIleIleValAlaPheGlySerLeu 968  
 DB 3532 GCATACAGATTTGAACCTTATTTGGTTCGTTATTTATTTGGCGCGCTGACTTTATCGGTT 3591  
 QY 969 IleLeuAlaLys-----ThrLeuAspAlaGlyGlnValGlyLeuAlaLeuSerTyrAla 986





OY	244	LeuLeileleuLeuProLeuGlnSerCybheGlyLysLeuPheSerSerLeuArgSer	263
Db	1366	CTAGTGGTAAAGAGCCATTAAATTCATTTTAAATGAATACAAAGAAATTAACAAAA	1425
OY	264	LysThrAlaThrPheThrAspAlaArgLLeaArgThrMetAsnGluValIlethnGlyIle	283
Db	1426	TCTCAAAATGAAGATACAAAGACGAAAGAACTGCTGTATTATGTGAATTCCTTAACAACTC	1485
OY	284	ArgIleIleLeuMetYrAlaTfPGLuLysSerPheSerAsnLeuIlethnAsnLeuArg	303
Db	1486	AAATCTCGAAATTAATATATGCGTGGGAAAGCCTTACACGGAGAAAGTTGGAAAGCGTTAGA	1545
OY	304	---LysTSGuIleSerLysIleLeuArgSerSerCybLeuArgGlyMetAsnLeuAla	322
Db	1546	AATAACAAAGAACCTAAATATTAATCTAAATTTGGGTGTCTATATGCTGTACAAAGTTCC	1605
OY	323	SerPhePheSerAlaSerLysIleIleValPheValThrPheThrYrValLeuLeu	342
Db	1606	CAATTTAACATAGTTCCTTCTCTAGTTTCAAGCTGTACGTTGGCTGTGTGTACACC	1665
OY	343	---GlySerValIlethnAlaSerArgValPheValIleValThrLeuYrGlyAlaVal	361
Db	1666	GAAGATAGGCGCTGACTACCGACTCTAGTTTCCCTGCTTAATCTTTCAATCTCACTT	1725
OY	362	ArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAlaIleVal	381
Db	1726	TCATTTCCATTTG---ATGATTATTCCCAATGTTTGAATTCATTTATTCGAAGCTTCGTT	1782
OY	382	SerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSer-----Gln	397
Db	1783	TCTATTTGGTAGCTATTTTCTTCTTTTTCACATAGAGAGCTACGACGATCTGTTCAG	1842
OY	398	ArgAsnArgGlnLeuProSerAspGlyLysLeuMetValHisVal---GlnAspPheThr	416
Db	1843	CGCTTACCAAAAGTAGAAATGTTGGTGATATACCATCAATATTGGCGACGACGCTACC	1902
OY	417	AlaPheTrpAspLysAlaSerGlu---ThrProThrLeuGlnGlyLeuSerPheThrVal	435
Db	1903	TTTTTATGCGACGTTAAACGAAATATATAGTACGTTGAAATAATATCAATTTCCAGCT	1962
OY	436	ArgProGlyGluLeuLeuAlaValValGlyProValGlyAlaGlyLysSerSerLeuLeu	455
Db	1963	AAGAAAGAGAAATTBACCTGTATTGTGTGGTAGAGGTGGTATGGGAAAGACCGCTCTATTA	2022
OY	456	SerAlaValLeuGlyGluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIle	475
Db	2023	TCAAGCAATTTGGGTGACTTATTATTAAGTCAAAAGGTTTGCTCAAGTGCACGAGTGT	2082
OY	476	AlaYrValSerGlnGlnProYrValPheSerGlyThrLeuArgSerAsnIleLeuPhe	495
Db	2083	GCATATCGTCTCACAAGTTCCATGATATATGATAGTAGGAGCGGTCAAGGAAACATTTGTGT	2142
OY	496	GlyLysLysYrYrGluLysGluArgTyrGluLysValIleLysAlaCybValAlaLeuLys	515
Db	2143	GGGCAATAGTACGAGTCTGACTTTATGAATAAACTATCAAGGCTGTGGGTATCCATT	2202
OY	516	AspLeuGlnLeuLeuGluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeu	535
Db	2203	GACTTGGGCAATTTTGATGTGATGGGTATAGACGCTAGTGGTGAAGAGGATTTCTCTG	2262
OY	536	SerGlyGlyGlnLysValaArgValAsnLeuAlaArgAlaValYrGlnAspAlaAspIle	555
Db	2263	TCGGGCGGCGCAAAAGGACGCTGTCTCTTACCAAGACAGCATGTTTTCAAAGGGCGAGATCT	2322
OY	556	TyrLeuLeuAspAspProLeuSerAlaValAspAlaGluValSerArgGlnIleuPheGln	575
Db	2323	TATCTACTGACGAGATCCCTTGCGGCTGTATACACACACGCGGTAGACATTTGTCTAAA	2382
OY	576	LeuCybIleCybGln-----IleLeuIleGluLysIleThrIleLeuValIlethnGln	593
Db	2383	CATGATATTGGGTCAAAATCGTTTACTACATTTCCAAAACCAAGTATTATGGACACGAACAA	2442
OY	594	LeuGlnYrLeuLysValaAlaSerGlnIleLeuIleLeuLysAspGlyLysMetValGln	613

[illegible]

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Db      3472 TGTCTATTGATTAATACATGAGTCGTTTATCTCTGTCATACGCTAATCGTTGGTTG 3531
Qy      949 AlAValArgLeuAspAlaIleCySaIaMetPheValIleIleValAlaPheGlySerLeu 968
Db      3532 GCATACAGATTGGAACCTTATGTTCTGTATATTTTGGGGCGCTACTTATTCGGTT 3591
Qy      969 IleuAlaIys-----ThrIeuAspAlaGlyIleValIleGlyLeuAlaLeuSerTyraIa 986
Db      3592 TTCAGGCTAAAGCAAGAGTACCTTGACCTGCGGGTATGCTGGTTGGCTGCTAAGTTATGCA 3651
Qy      987 LeuThrIeuMetGlyMetPheGlnTrpCysValArgIleSerAlaGluValAlaGluMet 1006
Db      3652 TTACAAATACCCAAACATTGAATGATGTTGATGATGATGATGATGATGATGATGATGATGAT 3711
Qy      1007 MetIleSerValIleuArgValIleGluTyThrAspLeuGluIleGluValAlaProTrpGlu 1026
Db      3712 ATGTGTTGGCTGAGAGATTAAGATACGCTGACTTAAAGATGAGCGCCCTTAACT 3771
Qy      1027 TyrgIn--LysArgProProProAlaTrpProHISgluGlyValIleIlePheAspAsn 1045
Db      3772 ATCGAAGGTACAGAGCCACCCAGGATGCGCAGGACCAAGTGCATCAAGTTCAATCA 3831
Qy      1046 ValAsnMetCysSerProGlyGlyProLeuValIleuIleHisIleuThrAlaLeuIle 1065
Db      3832 TATTCCTACTGTTATAGACCAAGCTTGATCTTGTCTGATAACAGATTGATATTCACATC 3891
Qy      1066 LysSerGlnGluIleValIleGlyIleValIleGlyArgThrGlyAlaGlyLysSerSerLeuIle 1085
Db      3892 AAACCGAAGGAAAAATTGGTATGTTGTTGATGACAGCGGCAAGTAACTCGTTAAACA 3951
Qy      1086 SerAlaIleuPheArgLeuSerGluProGlu--GlyLysIleTrpIleAspLysIleLeu 1104
Db      3952 TTAGCGCTATTCAGATCATTTAGCTAGTGCAGGAAATATGTTATGATGACATTCCTCC 4011
Qy      1105 ThrThrGlnIleGlyIleuHisAspLeuArgLysLysMetSerIleIleProGlnIlePro 1124
Db      4012 ATTAATGAATATGGGTTATATGATCTTAAGACATTAACCTGCTATTAATCTTCAAGATTC 4071
Qy      1125 ValIleuPheThrGlyThrMetArgLysAsnLeuAspProPheAsnGluIleHisThrAspGlu 1144
Db      4072 CAAGCTTTGAAGAGTACTGTTGCTGAGATATCGATCCATCAACCAATACACCGATGAG 4131
Qy      1145 GluLeuTrpAsnAlaLeuGlnGluValAlaGluLysGlyIleThrIleGluAspLeuProGly 1164
Db      4132 GCTATGTGAGAGCATTTGGAATCTTCTCATTTGAAGAACATGCTGTTATCATGAGTAAAC 4191
Qy      1165 Lys---MetAspThrGluIleuAlaGluSerGlySerAspPheSerValIleGlnArgGln 1183
Db      4192 GATGGGTATGACTCTCAATTAACAGAAAGGTGTAGTAACTTAAGTGTGAGCAAAAGACAA 4251
Qy      1184 LeuValCysLeuAlaArgAlaIleLeuArgLysAsnGlnIleLeuIleIleAspGluAla 1203
Db      4252 TTACGTGCTCTTCCGAGAGCAATGCTGTTCCATCCAAATTTTGGTCTGATGATGAGCC 4311
Qy      1204 ThrAlaAsnValAspProArgThrAspGluLeuIleGlnLysLysIleArgGluLysPhe 1223
Db      4312 ACCGCTGAGTGTGATGCTGAAACAGATAGATGATCAATCAAGACCAATTCGACGCGCTT 4371
Qy      1224 AlaHisCysThrValLeuThrIleAlaHisArgLeuAsnThrIleIleAspSerAspLys 1243
Db      4372 AGAGATAGAACTATATGTACTCTGACACAGAGTTGAAACCACTCATGATGACGATTAAC 4431
Qy      1244 IleMetValIleuAspSerGlyArgLeuLysGluTyArgAspGluProTyThrValIleuGln 1263
Db      4432 ATCATTTGTTGGATTAACGATTAAGTGGCTGAGTTGATTTCCCATCCCACTATTAAAC 4491
Qy      1264 AsnLysGluSerLeuPheTyThrLysMetValGlnGlnLeuGly 1277
Db      4492 AATACCAATCATTAATTCATTCGTTGTGACAGAAAGCCGGT 4533

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RESULT 14  
 US-11-136-527-2145  
 ; Sequence 2145, Application US/11136527

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; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2145
; LENGTH: 4954
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2145

Alignment Scores:
Pred. No.: 3,956-201 Length: 4954
Score: 2201.00 Matches: 495
Percent Similarity: 55.7% Conservative: 266
Best Local Similarity: 36.2% Mismatches: 478
Query Match: 32.4% Indels: 128
DB: 12 Gaps: 24

US-09-976-858-42 (1-1325) x US-11-136-527-2145 (1-4954)
Qy      12 ProLeuGlnAspAlaAsnLeuCysSerArgValPhePheTrpTrpLeuAsnProLeuPhe 31
Db      671 CCATGATGACAGCGCTCTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 730
Qy      32 LysIleGlnHisLysArgArgLeuGluIleuAspMetTySerValLeuProGluAsp 51
Db      731 CTGAAGGTTACAAACATCACTGACACTAGAAAGTCTGGGATATGATGATGATGATGATGATGAT 790
Qy      52 ArgSerGlnHisLeuGlyGluIleuGlnGlyPheTrpAspLysGluValLeuArgAla 71
Db      791 AAAACAGGTCACTCACCAGCAAGTTTGAAGCGGCATGACAAAGACCTTGCAAGAACCC 850
Qy      72 -----GluAsnAspAlaGlnLysProSerLeuThr----- 81
Db      851 AGCGAGGCTTTTCAAGAGCGGCTGCAAGATGCCAGGAAACCTTGAGGCCACACTACAC 910
Qy      81 ----- 81
Db      911 GGCATGAACAAGAACAGATGACAGCAAGACGTTCTGCTCGAAGAAAGCAAAAG 970
Qy      82 -----ArgAlaIleIleLysCysTyTrpLysSerTyLeuValLeuGlyIlePhe--- 98
Db      971 AAGTCTGAGAAAGCACCAAGCAATATCCCAATGCTGATGATCAAGTCTCTTCAAA 1030
Qy      99 -----ThrIleIleGluIleSerAlaLys 106
Db      1031 ACCTTCACGATGATCTGAAATCATTTATCTGAAATTAATTAATCAGACCTTTGGTG 1090
Qy      107 ValIleGlnProIlePheLeuGlyLysIleIleAsnTyPheGluAsnTyArgProMet 126
Db      1091 TTTCTGAATCTCCACCTGTGAAAGTGTGATGCTGATGCTTTC----- 1129
Qy      127 AspSerValAlaLeuAsnThrAlaTyArgLys-----AlaThrValLeuThr 142
Db      1130 -----GTGAAGAGCTTCAATCAATATGATGCTGTTGGCTATATATGTCATGCTTAATG 1183
Qy      143 PheCys---ThrIleIleuAlaIleuHisIleuHisIleuTyPheTyHisValGlnCys 161
Db      1184 TTGTGCTGACTCTATCCAAATCTTTCGCTTCACTTACTTCAACATGTTTGTG 1243
Qy      162 AlaGlyMetArgLeuArgValAlaIleMetCysHisMetIleTyArgLysAlaLeuArgLeu 181
Db      1244 TTGGGAATGTGCTAGCAACACCGTCAATGCTTGTGATATATGAAGACATGACCCCTTA 1303
Qy      182 SerAsnMetAlaMetGlyLysThrThrThrGlyGlnIleValAsnLeuLeuSerAsnAsp 201

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Db 1304 TCTAATCTGGCTAGAGACAGACAGTACCATTCGAGAGACGCTGACCTGCTGCTGAGT 1363  
 Qy 202 ValAaLysPheAaPglValThrValPheLeuH1sPheLeuThrAlaGlyProLeuGln 221  
 Db 1364 TCCCAAGAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1423  
 Qy 222 AlaIleAlaValThrAlaLeuLeuThrPheMetGlyIleGlyIleSerCybLeuAlaGlyMet 241  
 Db 1424 ATTACTTGTTCATCTTCTTCTGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1483  
 Qy 242 AlaValLeuIleIleLeuLeuProLeuGlnSerCybPheGlyLeuLeuPheSerSerLeu 261  
 Db 1484 GGGGTATAGCTTCTCTATCCCAAGTATATGAGATTCGCTGACCAAGATCAAGAAATAT 1543  
 Qy 262 ArgSerLysThrAlaThrPheThrAlaAlaArgIleArgThrMetAsnGluValIleThr 281  
 Db 1544 CAGGTCCCAAAATATGAAAGATTAAGCAAAACGTTTAAATCATGAAATGAGATTCAGAT 1603  
 Qy 282 GlyIleArgIleIleIleMetCysTrpAlaTrpGlyLysSerPheSerAsnLeuIleThrAsn 301  
 Db 1604 GGAATCAAGATCTGAAATATCTTGTGCTGAGAACTTCATTTCAAGACAACTCCAGGAG 1663  
 Qy 302 LeuArgLysLysGlyIleSerLysIleLeuArgSerSerCysLeuArgGlyMetAsnLeu 321  
 Db 1664 ATTCGAGAAAGAAAGAACTCAAGAACTTCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAG 1723  
 Qy 322 AlaSerPhePheSerAlaSerLysIleIleValPheValIleThrThrThrThrThrValLeu 341  
 Db 1724 TTCATTTTACAGATAATCCAAATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1783  
 Qy 342 LeuGlySer-----ValIleThrAlaSerArgValPheValAlaValIleThrLeuArgly 359  
 Db 1784 GTGATGAGGCAATGTTTGAATGCGAAGAGCAATTAATCTCCATCCATCCCTCTTCAT 1843  
 Qy 360 AlaValArgLeuThrValThrLeuPhePheProSerAlaIleGluArgValSerGluAla 379  
 Db 1844 ATCTTAAGCTTCCCTCTGTCATG---CTTCCATGATGATGATGATGATGATGATGATGAT 1900  
 Qy 380 IleValSerIleArgArgIleGlnThrPheLeuLeuLeuAspGluIleSerGlnArgAsn 399  
 Db 1901 AGTGTTCCTGAGACCGGCTGAGAGATTTGGAGAGAGACGATTTAGACATCTGAGC 1960  
 Qy 400 ArgGlnLeuProSerAspGlyLysMetValHisValGlnAspPheThrAlaPheTrp 419  
 Db 1961 ATTCCCGGCTGAGCAATTTGATTAAGCTGTAAGCTTTCAAGAGGCTCTTTACTTGG 2020  
 Qy 420 AspLysAlaSerGlyThrProThrLeuGlnGlyLeuSerPheThrValArgProGlyArg 439  
 Db 2021 GACCCGAGCTTGAAGCC---ACATCCAAAGATGTAACCTGACATTAAGCCAGGCCAA 2077  
 Qy 440 LeuLeuAlaValAlaGlyProValGlyAlaGlyLysSerSerLeuLeuSerAlaValLeu 459  
 Db 2078 CTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2137  
 Qy 460 GlyGluLeuAlaProSerHisGlyLeuValSerValHisGlyArgIleAlaIleArgValSer 479  
 Db 2138 GGAAGAAATGAAACGTTTACCGGACATCACCATTCAGGATCCACACCTATGTCCT 2197  
 Qy 480 GlnGlnProTrpValPheSerGlyThrLeuArgSerAsnIleLeuPheGlyLysLysTrp 499  
 Db 2198 CAGCGATCTGATTCAGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 2257  
 Qy 500 GlyLysGluArgTrpGlyLysValIleValAlaCysValLeuLysLysAspLeuGlnLeu 519  
 Db 2258 AATGAAAGAGATCAAGCAAGTTCTCAAGCATGCTCTCTCCCAAGATCTTGAAATA 2317  
 Qy 520 LeuGluAspGlyAspLeuThrValIleGlyAspArgGlyThrThrLeuSerGlyGlyGln 539  
 Db 2318 TTGGCTGAGAGACATGCTGAGATCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2377  
 Qy 540 LysAlaArgValAsnLeuAlaArgAlaValIleTrpGlnAspAlaAspIleTrpLeuLeuAsp 559

Db 2378 AAGCAGGATGACGCTGCGCCAGAGCTGCTATCAAGATGCTGACATCATATATCTGAGC 2437  
 Qy 560 AspProLeuSerAlaValAspAlaGlyValSerArgHisLeuPheGlyLeuCysIleCys 579  
 Db 2438 GATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2497  
 Qy 580 Gln-----IleLeuH1sGlyLysIleThrIleLeuValIleThrIleGlnLeuGlnTrpLeu 597  
 Db 2498 CCCAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2557  
 Qy 598 LysAlaAlaSerGlnIleLeuIleLeuLysAspGlyLysMetValGlnLysGlyThrTrp 617  
 Db 2558 CCCCAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2617  
 Qy 618 ThrGluPheLeu---LysSerGlyIle-----AspPheGlySerLeuLeuLysLys 633  
 Db 2618 CGTGAACCTGTTGAGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2677  
 Qy 634 AspAsnGluGluSerGluGln----- 640  
 Db 2678 TCAGGCGCTGAAGAT 2737  
 Qy 641 -----ProProValProGlyThrPro----- 647  
 Db 2738 GGGCTGATTTCCACATGAGAGAAATCCCTGAGATGACGCTTCTGCGCATGAGAGA 2797  
 Qy 648 -----ThrLeuArgAsnArgThrPheSerGluSerSerValIleTrpSerGlnIleSer 665  
 Db 2798 GAAATATGCTTCCTGCG---CGTACACTGAGCGGACAC-----TCAAGTCCAGCAGC 2845  
 Qy 666 Arg-----ProSerLeuLysAspGlyAlaLeuGluSerGlnAspThrGluAsnValPro 683  
 Db 2846 CACCTGAGAACTCCCTCAAAAC-----TCTTGAAGATTTAAATGTGAAAT 2893  
 Qy 684 ValThrLeuSerGluGluAsnArgSerGlu----- 693  
 Db 2894 GTCTTGAAGAT 2953  
 Qy 694 -----GlyLysValGlyPheGlnAlaIleArgLysAsnTrpPheArgAlaGlyAlaHisTrp 711  
 Db 2954 GAAACCGGAGAGAGTCAAGTTCTCCATCTCAAGATGATCAAGAGAGAGAGAGAGAGAGAG 3013  
 Qy 712 IleValPheIlePheLeuIleLeuLeuAsnThrAlaIleAlaIleValIleValLeuGln 731  
 Db 3014 TCCATA---CTTTATCATCTTTTCAAGATGAAATATGTTGCTTTATCGGCTCT 3070  
 Qy 732 AspTrpTrpLeuSerTrpAlaAsnLysGlnSerMetLeuAsnValThrValAsnGly 751  
 Db 3071 AACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3118  
 Qy 752 GlyGlyAsnValThrGlyLysLeuAspLeuAsnTrpTrpLeuGlyIleLysSerGlyLeu 771  
 Db 3119 ACCAAACAATGCTCTTCAATGAGACATGAGA-----ATTGGGCTCTTGGAGCTGCTG 3172  
 Qy 772 ThrValAlaThrValLeuPheGlyIleAlaArgSerLeuLeuValPheTrpValLeuVal 791  
 Db 3173 GGATTAAGCAAGATATATGTTTGTCTTATTTCAACTCTGTGAGCATATATCTTGCACA 3232  
 Qy 792 AsnSerSerGlnThrLeuH1sAsnLysMetPheGluSerIleLeuLysAlaProValLeu 811  
 Db 3233 AATGATCAAAAGCTTTCAGAGGCGAGCGGTTAAACCAATCTCTCGGAGCAACCATGAGG 3292  
 Qy 812 PhePheAspArgAsnProIleGlyArgIleLeuAsnArgPheSerLysAspIleGlyHis 831  
 Db 3293 TTTTGTGACAACTCCCAAGCGCGGATTTGAAACAATTTCTGATATTTCTACT 3352  
 Qy 832 LeuAspAspLeuLeuProLeuThrPheLeuAspPheIleGlnThrLeuGlnAlaVal 851  
 Db 3353 GTGAGCACTGCTCTCCCAAGCACTTGAAGCTGAGATGCTGTTCTTGGCATCGCT 3412  
 Qy 852 GlyValAlaSerValAlaValAlaValIleProTrpIleAlaIleProLeuValProLeu 871  
 Db 3413 GGCACCTCTTGTATCATGATCGATGCGACCCAGCTTCGGTATCATCATCTCTCTC 3472

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QY      872  GIIYLEIEPHEIIEPHELEUARGRYRPHLEUGLUTHSERARGSPVALIYSARG      891
      |||.....|||.....|||.....|||.....|||.....|||.....|||.....|||
Db      3473  AACATCTTATATATTCGGTGACAGGTTTATTATGTGCTACTTCCGCGACGTGACAGG      3532
QY      892  LEUGLUSERTHTRARGSERPROVALPHESEHISLEUSERSERIEUGLNUYLEU      911
      |||.....|||.....|||.....|||.....|||.....|||.....|||.....|||
Db      3533  TTGGATTCTGTACCAAAATCTCGATCTCTCATCTTCAGTACAGCTCTCCAGGTTTG      3592
QY      912  TPTTHIIEARGALATRYLSALAGLUGIUAIRGYSGLINGLULEUPHEAPLAHISGLIN      931
      |||.....|||.....|||.....|||.....|||.....|||.....|||.....|||
Db      3593  CCCATTATCCGTCGCTTTAGACACCAAGCCGATTTCTAGCTTGGAATAGAAAGCAGATT      3652
QY      932  AAPLEUHSISERGLUALATRPHELEUPHELEUTHTRHSERARGTRPHEALAAVALARG      951
      |||.....|||.....|||.....|||.....|||.....|||.....|||.....|||
Db      3653  GACATCAACCAAGAAATGTCTTTCTCGATTAATCTCCAAACAGGTCGTCGAATTCGG      3712
QY      952  LEUAPALAIIECYALAMETHEVALIIEILEVALIAPHEGLYSERIEULEUALA      971
      |||.....|||.....|||.....|||.....|||.....|||.....|||.....|||
Db      3713  CTGGAGCTGGTTGAAACTTGTCCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG      3772
QY      972  LYSTHTRLEUASPALAGLYGLINVALIIELEUVALALEUSERTRYALALEUTHRIEUGLY      991
      |||.....|||.....|||.....|||.....|||.....|||.....|||.....|||
Db      3773  AAAACCTTAACCGGAGCGGAGCTGTGGCTTTGCTTCTCTCAACGCCCTCAATATCACAA      3832
QY      992  METPHEGLNTRPCYSVALARGINSEALAGIUALIIEUASMETMETIIESEVALGIU      1011
      |||.....|||.....|||.....|||.....|||.....|||.....|||.....|||
Db      3833  ACCTTGAACCTGGCTAGTGAGATGACGTCAAGACAGAACCAACATTGTGGCAGTTGAG      3892
QY      1012  ARGVALIIEGLUTRYTHRASPHEUGIULYSGIUALAPROTRIGLUTRYGLINLYSARG      1031
      |||.....|||.....|||.....|||.....|||.....|||.....|||.....|||
Db      3893  CGAATTAAGTAATACCTAATATAGAGAAAGAGGCCCTCGGTGAGTACAGAGGCCCT      3952
QY      1032  PROPROALATRPROIHISGLUGIYVALIIEIIEPHEAPSPVALIIEPHEMETTYRSE      1051
      |||.....|||.....|||.....|||.....|||.....|||.....|||.....|||
Db      3953  CCGGACGACTGGCCGACAGATGTGAGATCCAGTTTAACTATCAAGTCCGATTCGG      4012
QY      1052  PROGLIYGLIYPROLEUVALIIEULYSLEUTHRALALEUIELYSERGLINGIULYVAL      1071
      |||.....|||.....|||.....|||.....|||.....|||.....|||.....|||
Db      4013  CCGGAGCTGGATCTGTGTAAGGAGATCATCTTGAACATCAAGACGCGAGAGAGGTC      4072
QY      1072  GIYIIEVALIIEGLYARGHTRGLYALAGIYLYSERSEIEULESERIALALEUPHEARGLEU      1091
      |||.....|||.....|||.....|||.....|||.....|||.....|||.....|||
Db      4073  GGCRTTRGTGGSGMGAAGCTGGGCTGGGAATCATCCCTACRARSCTCTTCGAAATC      4132
QY      1092  SERGLUPROGLU---GLYLSIIEETRPILASPLYIIELEUTHRGLINLEUGLYLEU      1110
      |||.....|||.....|||.....|||.....|||.....|||.....|||.....|||
Db      4133  TTAGAGTCTGGGGGGGCGACATCATATTGATGGATGAGTTCCTCCATTGGACTG      4192
QY      1111  HISAPLEUARGIYLYSEMERSEIIEIIEPROGLINGLUPROVALLEUPHEHTRGLYTH      1130
      |||.....|||.....|||.....|||.....|||.....|||.....|||.....|||
Db      4193  CACGACCTTCGAGAGAGGCTGACATCATTTCCCAAGACCCATTGTTCTCGGGAGCT      4252
QY      1131  METARGLYASMLEUPROPHESANGIULHISHTHARGGLUGIULEUTHRPHENALALEU      1150
      |||.....|||.....|||.....|||.....|||.....|||.....|||.....|||
Db      4253  CTGAGGATGAATCTCAACCTTTTCACAAATATTCAGATGAGAGGTTTGAGGGGCTCG      4312
QY      1151  GINGIULVALIIEULEUSGLIUTHRIIEGLIUALASPLEUPROGLIYLYSEMERAPHTRGLI      1170
      |||.....|||.....|||.....|||.....|||.....|||.....|||.....|||
Db      4313  GAGTTGGCTCACTCGATTCCTTGTGTCTGCGCTTACAGTGGGTGTTGATTCGAAGTG      4372
QY      1171  ALAGIUSERGLYSEANPHESEVALIIEGLINARGIULEUVALICYSEUVALIARGALA      1190
      |||.....|||.....|||.....|||.....|||.....|||.....|||.....|||
Db      4373  ACAGAGGCTGTGACAACTGAGCATATGAGGACAGGCACTCTTATGCTCGGGCAGGGCT      4432
QY      1191  IIELEUARGLYASMLEUINIELEUIEILEAPGLUALATHRALAASVALIAPPROARG      1210
      |||.....|||.....|||.....|||.....|||.....|||.....|||.....|||
Db      4433  GTGCTTCAAAAATCCAAAATCTGTGCTCTGATGAAAGCCACGCTCAGTGGATCTCGAG      4492
QY      1211  THRAPGLULEUIIEGLINLYSLSIIEARGGLIULYSPHEALAHISGYETHRALLEUTH      1230
      |||.....|||.....|||.....|||.....|||.....|||.....|||.....|||
Db      4493  ACGGATGCTCTATCAAGACCATCCAAAGAGATCTCCAGTGCACGGKCATCACCC      4552

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QY      1231  IIEALAHISARGLEUASHTHRIIEIIEAPSERAPPLYIIELEUVALIIEUPSERGLY      1250
      |||.....|||.....|||.....|||.....|||.....|||.....|||.....|||
Db      4553  ATTCCTCAACAGCTGACACACATCATGACAGTGACAAAGATATGTCCTTACACACGG      4612
QY      1251  ARGLEUYSGLIYTRASPGLUPROBYRVALLEUGIULANULYGLUSERLEUPHETRY      1270
      |||.....|||.....|||.....|||.....|||.....|||.....|||.....|||
Db      4613  AAGATTGCGAGTATGAGCAGTCTCAAGAAATCTGTCTCAACAGAGTTCC---TTCTAT      4669-
QY      1271  LYSMETVALINGLINGLEUGIY      1277
      |||.....|||.....|||.....|||.....|||.....|||.....|||.....|||
Db      4670  CTGATGGCAAGAGGACCGGC      4690

RESULT 15
US-11-136-527-475
; Sequence 475, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 475
; LENGTH: 5189
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-11-136-527-475

Alignment Scores:
Pred. No.:      1,7e-198      Length:      5189
Score:          2174.00      Matches:      484
Percent Similarity: 56.1%      Conservative: 277
Best Local Similarity: 35.7%      Mismatches:  485
Query Match:     32.0%      Indels:      110
DB:              12          Gaps:          24

US-09-976-858-42 (1-1325) x US-11-136-527-475 (1-5189)
QY      3  PROVALIYRGINGIULVALIIEPHEAPSPVALIIEPHEMETTYRSEARGVAL      22
      |||.....|||.....|||.....|||.....|||.....|||.....|||.....|||
Db      658  CCAGAGAAATCTTGACAAATCTCTGCGACAGGCGCTGCTTCTTCCCGTCTG      717
QY      23  PHEPETHPTPLLEUASNPPOLEUPHELYSIIIEGLIYHSIYARGARGLEUGIULASP      42
      |||.....|||.....|||.....|||.....|||.....|||.....|||.....|||
Db      718  TCTTCTGCTGTGTTCAAAAGCTTGCATCTTGGCTACCAAGCTCCCTGAGGACAGT      777
QY      43  APMETTRYSERVALIIEUPROGLIULASPARSERGINHISLEUGIULUGIULEUGLINGLY      62
      |||.....|||.....|||.....|||.....|||.....|||.....|||.....|||
Db      778  GACCTCTGTCTCTGTCTGAGAGGACTGCTCTCAAGAGTGCTCAACGCTTACTGGAA      837
QY      63  PHETRAPPLYSGLU-----        67
      |||.....|||.....|||.....|||.....|||.....|||.....|||.....|||
Db      838  GGATGCAAAAGACACAGACCAAGCATCAGGCCCCCAGACTGACGCTTGAAGCAAG      897
QY      68  -----VALLEUARGIAGIULASNPALAGIULYEPROSERLEU      80
      |||.....|||.....|||.....|||.....|||.....|||.....|||.....|||
Db      898  ATCGAGGTGAGATGAGGTCTGCTGAAGCGCCGCCCAAGACCAAGAGCTTCTTT      957
QY      81  THARGALAIIEIIELYSCYETRYTRPYSERYTRYLEUVALIIEUGIYIIEPHEHTRLEU      100
      |||.....|||.....|||.....|||.....|||.....|||.....|||.....|||
Db      958  CTGAGGCTTGTGTAGAACCTTCACTCCAGCTTCTCATAGGGTCCCTGCTCAAGCTG      1017
QY      101  IIEGLIUSERALALYVALIIEGLINPROIIEPHELEUGIYLYSIIIEASNTYRPE      120
      |||.....|||.....|||.....|||.....|||.....|||.....|||.....|||
Db      1018  ATCCAGGACCTGCTCTCTTATCAACCAACCAAGCTGCTCAGATCTCATGAGTTTAT      1077
QY      121  GIUAENTYRASPROMETAPSPSERVALIIELEUASHTHRIIEA-----TYR      135
      |||.....|||.....|||.....|||.....|||.....|||.....|||.....|||

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QY	806	LeuValSerProValLeuPhePheAspArgAnpProIleGlyValLeuAsnArgPhe	825
Db	3208	ATCGGCGGCGCTCATCTCTTTGACACAGAGCGCTTAGGCGCGCATCTCAATCGTTTC	3267
QY	826	SerIlyAspRIleGlyHisLeuAspAspLeuPheLeuThrPheLeuAspPheIleGln	845
Db	3268	TCCAAGACATATAGCATGATCATGATGAGTTCTGGCCCCCACCACATCTCATGCTGTTCAT	3327
QY	846	ThrIleuLeuGlnValValGlyValValSerValAlaValAlaValIleProThrIleAla	865
Db	3328	TCATTTCTACATCCATCTCCACCACTTGTGGTCATCGTGGCCAGACCGCACTCTTCTGC	3387
QY	866	IleProLeuValProLeuGlyIleIlePheIlePheLeuAspArgGlyPheLeuGlnThr	885
Db	3388	GTGGTTGTTCTCTCTCTGGCTGTGTGTTCTTAGGCTTTGCGACGCGTTTATATGGCCACA	3447
QY	886	SerArgAspValIlySargLeuGlnSerThrThrArgSerProValPheSerHisLeuSer	905
Db	3448	TCGAGGCGAGCTGAAGAGATCGGAATCGGTAGCGCGCTGCCCATCTTCTCCACGTTCTCG	3507
QY	906	SerSerLeuGlnGlyLeuThrThrIleArgAlaIlyTlyValAGluGlnArgCysGlnGlu	925
Db	3508	GAGACAGTAATCGGACCAAGTCATTCGCGGCTTAGCGCCAGACGTCACAGCTTCAAGCTC	3567
QY	926	LeuPheAspAlaHisGlnAspLeuHisSerGlnIlyAlaThrPheLeuPheLeuThrThrSer	945
Db	3568	CTCACTAGTATGGTAAAGTGATAGCAACAGAAAGCACTTATCTTACATGCGCTCCCAAC	3627
QY	946	ArgTrpPheAlaValArgLeuAspAlaIleCysAlaMetPheValIleIleValAlaPhe	965
Db	3628	CGGTGCGCGGGGTCACGTGGAGTTTGTGGGAATCGCGTGGCTCTTCTCGCGCGTG	3687
QY	966	GlySerLeuIleLeuAlaIlyThrLeuAspAlaGlyGlnValGlyLeuAlaLeuSerTyr	985
Db	3688	TTTGCAGTAGATCGGAGAAACAGCTTGAATCCAGGCGCTTGTGGCTTCCGTGCTCAT	3747
QY	986	AlaLeuThrIleuMetGlyMetPheIleThrCysValArgGlnSerAlaGlnValGlnAsn	1005
Db	3748	GCTTTACAGGATGCTTAGTTGAATTGGATGATAGCAAGCGTATCCGACCTGGAGTCT	3807
QY	1006	MetMetIleSerValGluArgValIleGluTyrThrAspLeuGluValAlaProThr	1025
Db	3808	AATATCAATGCCGTGGAGAGAGTCAAGAGATCTTAAGACGAGACCTGAGGCTCCCGG	3867
QY	1026	GluTyrGln--LysArgProProAlaIaTrpProHisGluGlyValIleIlePheAsp	1044
Db	3868	GTGTTGGAGACCAACCTGTCTCCAGAAAGCTGGCCCAAGAGGGGTGTGAGATTCCGG	3927
QY	1045	AsnValAsnPheMetTyrSerProGlyIlyProLeuValIleuValHisLeuThrAlaLeu	1064
Db	3928	AACATATGGTGGCGGTACCGCCCGCGGCTCGCAGTTGGTGTGAAATTTACCTCGCAT	3987
QY	1065	IleIlySerGlnGluValValGlyIleValGlyArgThrGlyAlaGlyLysSerSerLeu	1084
Db	3988	GTGACGGGTGGGAGAAAGTAAAGCATCTGGGCGGCACCTGGGCGCGAAATTTTCATG	4047
QY	1085	IleSerAlaLeuPheArgLeuSerGlu--ProGlnGlyIlySileThrIleAspIlyIle	1103
Db	4048	ACTCTTTCCTATTTCCGAATCTCGGAGCGCGAGAGGGGTGAATCTTCAATGAGGGCTC	4107
QY	1104	LeuThrThrGlnIleGlyIleuHisAspLeuArgIlySlySmetSerIleIleProGlnGlu	1123
Db	4108	AATGTGGACACATTTGGGCTCCATGACCTTGCGTTTCAACATCCATATCCCTCAGGAC	4167
QY	1124	ProValIleuPheThrGlyThrMetArgIlyAsnLeuAspProPheAsnGlnHisThrAsp	1143
Db	4168	CCCATCTCTGTTCTCGGACGCTGTGGCAATGAATCCCTTGATCCCTTGGCCGTATCTGGAC	4227
QY	1144	GluGluLeuThrPAsnAlaLeuGlnGluValAGlnLeuIlySgIuThrIleGluAspLeuPro	1163
Db	4228	GAGACATCTTGAGAGACCTGTGAGCTATCCACCTGATGTCATTTGTGAGACGACGCGG	4287
QY	1164	GlyIlySmetAspThrGlnLeuAlaGlnSerGlySerAsnPheSerValGlyGlnArgGln	1183

Db	4288	ACAGCGCTGGATTTTCA	GTGCTCGAGGGGTATATCTCA	GTGTGGCCAGAGCAG	4347
Qy	1184	LeuValLysLeuValaIaIgaIall	LeuValGlyAsnGlnIleLeuIleIleAspGluAla		1203
Db	4348	CTCTGTGGCTTAGCCGAC	CGCCGTGCTCCGAAAGAGCGCGTCTCGTGTTTTAGACAGAGCC		4407
Qy	1204	ThrIleAsnValAspProA	rgTThrAspGlnLeuIleGlnIlyLysIleArgGluValyPhe		1223
Db	4408	ACCGCTCCCATGTGAC	CTGGAGACTGTAAGACTTATCCAGGGTACCATCCGTACCCAGCTTT		4467
Qy	1224	AlaHisCysThrValIleu	ThrIleAlaHisArgLeuAsnThrIleIleAspSerAspLys		1243
Db	4468	GAGACCTGCACCTGACT	GACCAATCGCCACCGGCTCAACCAATCANTGAGCTACAAACCG		4527
Qy	1244	IleMetValLeuAspSerGly	IaIaGlyLeuGlnIuIyTrAspGluProGlyValIleLeuGln		1263
Db	4528	GTCCTGTCTTTGGCA	AAAGAGTAGTGTGCAATTTGATCTCCAGTAAACATCTCATTTGCA		4587
Qy	1264	AsnIlySerIuSerLeuPheTy	rIlySerValGlnGlnLeuGlyLysAla		1279
Db	4588	---GCTGAGAGCACTT	CTATGGAGATGGCCAAAGATGACAGACTCGCC		4632

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